From: Sent:

Bugaisky, Gabriele

Sent: To: Wednesday, January 08, 2003 1:29 PM STIC-Biotech/ChemLib

Subject:

09/943692

please search SEQ ID NO:2 and truncations thereof >530 aa.

thanks, gabi

Gabriele E. Bugaisky

- * au 1653
- * cm1-10d09; mailbox 9b01
- * 308-4201

truncations >530 should be truncations the standard search.

retrieved in the standard search.

retrieved in the standard search search towever, I thought an oligomer search wouse to the poly, since it provides might also be helpful, since it provides are might also be helpful, since it provides are might also be helpful, since it provides are might also be that contains contrains are that are might also be that are guery sea. Hits are 100% matches to the guery of the length to 100% match sequences in the length of the length of

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: Both
Phone:
Location:
Date Picked Up:
Date Completed: 1-10-03
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

/ENDOR/COST (where applic.)
STN:
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AAP82487
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AAP94679
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Delta endotoxin en
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B.t.t. coleopteran
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Bacillus thuringie	AAW00334	17	597	٢	3149
An artificial modi	AAW34784	18	645	7.	3328
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	-	18	644	9	3392
us thurin	AAP80467	ø	644	99.7	3396
_	AAW34838	18	644	9.	3397
Novel	AAW34837	18	644	9	3397
Novel C	AAW34811	18	644	9	3397
Novel	AAW34839	18	644	9	3398
Novel	AAW34833	18	644	9	3398
Novel	AAW34831	18	644	9.	3398
Novel	AAW34824	18	644	9	3398
Novel	AAW34823	18	644	9	3398
Novel	AAW34816	18	644	9	3398
Novel	AAW34815	18	644	9	3398
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Novel	AAW34825	18	644	9	3400
Novel CryIIIA	AAW34821	18	644	۰	3400
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Novel CryIIIA	AAW34813	18	644	9.	3400
Novel CryIIIA	AAW34836	18	644	٩	3401
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	AAW34834	18	644	۰	3401
Novel CryIIIA muta	AAW34832	18	644	۴	3401
Novel Cryllia	AAW34820	18	644	۰	3401
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Novel CryIIIA	AAW34828	18	644	٠	3402
Novel CryIIIA	AAW34822	18	644	. ه	3402
Novel Cryllia	AAW34841	18	644	۰.	3403
Novel CryIIIA	AAW34829	18	644	99.9	3403
Novel	AAW34827	18	644	۳	3403

ALIGNMENTS

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RESULT 1
AAP70085
 Sequence of toxin which is toxic to beetles of the order Coleoptera.
                                                                                                                                                                                                                                      04-MAY-1991 (first entry)
                                                                                                                                                                                                                                                        AAP70085;
                                                                                                                                                                                                                                                                         AAP70085 standard; Protein; 644
New poly:peptide toxin having pesticidal activity - formed by bacillus thuringiensis toxin gene, and useful for killing
                         WPI; 1987-066492/10
N-PSDB; AAN70092.
                                                                                        16-JUN-1986;
16-AUG-1985;
                                                                                                                  08-AUG-1986;
                                                                                                                                     11-MAR-1987.
                                                                                                                                                      EP213818-A.
                                                                                                                                                                      Bacillus thuringiensis
                                                                                                                                                                                        Microbial pesticide.
                                                     Herrnstadt C, Wilcox E;
                                                                      (MYCO-) MYCOGEN CORP.
                                                                                        86US-0874727
85US-0767227
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RESULT 2
AAP82487
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Best Local
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         Bacillus thuringiensis
                                 Coleoptera; toxin; cryC; insecticide;
                                                                                     01-NOV-1990
                                                                                                                                    AAP82487 standard;
                                                                                                              AAP82487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B. thuringlensis toxin gene toxic to Coleoptera beetles is cloned and expressed. Live micro-organisms for inhibiting the growth of, or killing, the beetles are obtd. The polypeptide toxin may be isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for use against the beetles.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
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                                                                                                                                                                                                                                                                                                                                           KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               644;
                                                           endotoxin
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                                                                                  (first entry)
                                                          encoded by cryc
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Pred. No. 1.7e-268;
0; Mismatches 0;
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                                delta-endotoxin;
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Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The cryC gene encodes a delta endotoxin which is an insecticide effective against Coleoptera and Lepidoptera. The sequence was isolated from cDNA library, on a plasmid designated pEC212. The plasmid can be used to construct an expression vector which can be used to transform B. megaterium ATCC 35985. Colorado potato beetle larvae treated with a suspension of cultured cells were dead within one week. The protein can be used as pure crystals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New gene encoding delta endotoxin of Bacillus thuringiensis effective as insecticide against Coleoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1988-338229/47.
N-PSDB; AAN82139.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Donovan WP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ECOG-) ECOGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-1987;
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                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in the form of B.t.
                                                                                                                                                                         KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
                                      GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT
                                                                        DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                                                                                                      DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                         GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT
                                                                                                                                                                                                                                          IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
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                                                                                                                                                                                                                                                                                                                                                                                                                              644 AA;
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Pred. No. 1.7e-268;
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644 AA;

Query Match Sequence

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       The btl3 gene encodes a 66 kDa crystal protein (the Btl3 protein) which is believed to be the active protein in the crystal toxin (the Btl3 toxin) produced by Bacillus thuringlensis (B.t.) tenebrionis and B.t. Sl. The patent is for a transformed plant cell which includes, inserted in its genome, the btl3 gene, or a fragment which encodes the 66kD crystal protein. Plant cells conts. DNA encoding this protein are protected against Choleoptera. Also new are plants (and their seeds) conts, these cells; a specific DNA sequence of 1760 b; the crystal protein; and microorganisms transformed with the DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus thuringiensis tenebrionis; 66 kDa crystal protein; Bt13 protein; toxin; Coleoptera; pTVE38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP94679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP94679 standard; protein;
                                                                                                                                  Disclosure; ; 35pp; English.
                                                                                                                                                           Coleoptera pests
                                                                                                                                                                     Plant cell transformed with DNA - is for Bacillus thuringiensis tox
                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                               Vaeck M, Hofte H,
                                                                                                                                                                                                                                                                      (PLAN-)
                                                                                                                                                                                                                                                                                               29-DEC-1987;
                                                                                                                                                                                                                                                                                                                      15-AUG-1988;
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                                                                                                                                                                                                                                                                       PLANT GENETIC SYSTEMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="N-terminal residues of the Bt13 protein" 5\theta
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="This residue was not unambiguously determined
it could possibly be Ser."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                               Botterman
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                                                                                                            M-7 toxin crystal; Coleoptera; beetle
                                                                                                                               M-7 crystal
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                                                                                                                                                   08-AUG-1990 (first entry)
                                                                                                                                                                                            AAP95585 standard;
                                                  01-AUG-1989
                                                                                        Bacillus thurigiensis strain
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16-AUG-1985;
15-JUL-1988;
                             30-NOV-1988;
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85US-0767227
88US-0219420
                             88US-0278292
                                                                                                                                                                                           protein;
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Pred. No. 1.7e-268;
                                                                                         san-diego
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RESULT 5
AAR39751
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Best Local
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              AAR39751;
                                      AAR39751 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The gene encoding the toxin can be cloned and used to produce the M-7 crystal which has activity against eg western spotted cucumber beetle, and northern, western and southern corn rootworm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ing of Bacillus thuringiensis toxin gene expression of protein toxic to beetles of
                                                                                                                         YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
                                                                                                                                                                              TENGSAATIYYTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
                                                                                                                                                                                                                                  MOGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC 540
                                                                                                                                                                                                                                                                                           KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
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                                                                                                         YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
                                                                                                                                                                TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
                                                                                                                                                                                                                   MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
                                                                                                                                                                                                                                                                            KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
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                                                                                                                                                                                                                                                                                                                                                                                      DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DHCVKWYNVGLDKLRGSSYESWVNFNRYRREWTLTVLDLIALFDLYDVRLYPKEVKTELT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1989-277854/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     644;
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                                       Protein;
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Pred. No. 1.7e-268;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Many strains of Bacillus thuringiensis (B.t) produce insecticidal delta endotoxins. A number of these endotoxins have been found to be toxic to Damilinia ovis, the biting louse of sheep. The B.T. isolates which produce these toxins can be grown and the delta endotoxin which is produced can be recovered by standard procedures. The genes encoding these endotoxins can also be transferred to a suitable host via a recombinant vector and the resulting transformants used in methods to control lice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 31-32; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Controlling biting lice on sheep - cor Bacillus thuringiensis toxins to host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                 GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT
                                                                                RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLEDYLHRIQFHTRFQPGYYGNDSFNYWS
                                                                                                                                        DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                                                                                                                       DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                                                                                                                                                                               MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
                                                                                                                                                                                                                                                                      IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
                             GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT
                                                                                                                                                                                                MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
                                                                                                                                                                                                                                                     TADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
                                                                                                                                                                                                                                                                                                           TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
                                                                                                                                                                                                                                                                                                                           TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDOK 120
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DB; AAQ47288.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    644 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus; lice; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Payne J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92US-0828788
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                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 3406; DB 14;
Pred. No. 1.7e-268;
Mismatches 0;
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Matches
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11-JUL-1989;
28-AUG-1991;
26-FEB-1993;
                                                                                           This sequence shows the amino acid sequence of CrylIIA protein. The promoter from the CrylIIA gene sequence was fused to the protein coding region of the CryBII gene (AAQ71027). The recombinant hybrid fusion gene expressed the CryBII crystal protein more efficiently than its native promoter. CryIIB encodes an insecticidal crystal protein isolated from Bacillus thuringiensis var. kurstaki. It produces crystal proteins during sporulation which are specifically toxic to certain orders and species of insects, esp. Lepidopterans. CryIIB can be used in compositions used as environmentally acceptable insecticides. (See also AAR56696 and AAR56698)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CryIIA; CryIIIA; CryIIB; CryC; P-2; CryBI; insecticidal protein crystal;
lepidoptera; environmental insecticide; Bacillus thuringiensis; toxic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CryIIIA insecticidal crystal protein.
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                                                                                                                                                                                                                                                                                                                                                                 (ECOG-)
                                                                        Sequence
                                                                                                                                                                                                                                       Example 7; Fig 4A-4D; 39pp; English.
                                                                                                                                                                                                                                                              thuringlensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS
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                                    Similarity
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                                                                                                                                                                                                                                                              protein - obtd. from the cry II B gene in Bacillus
is var. Kurstaki, active against lepidopteran insec
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89US-0379015.
91US-0751452.
93US-0023736.
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Pred. No. 1.7e-268;
Mismatches 0;
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26-FEB-1993;
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probe; hybridisation.
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                        (ECOG-) ECOGEN
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                                                                    87US-0039542.
89US-0379015.
91US-0751452.
93US-0023736.
                          INC
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                                                                                                                                                                                                                                                                                                                                                                                              CryC; P-2; CryBI; insecticidal protein crystal;
al insecticide; Bacillus thuringiensis; toxic;
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Best Local S
Matches 644
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                                                                                                                      481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Cry IIB protein - obtd. from the cry II B gene in Bacillus thuringiensis var. Kurstaki, active against lepidopteran insects
                                                                                         541
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                                                     MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
                                                                                                                                                                                        KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
                                                                                                                                                                                                                                GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT
                                                                                                                                                                                                                                               GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT
                           YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
                                                                                                                MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
                                                                                                                                                                       KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
                                                                                                                                                                                                                                                                                        RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS
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                                                                                                                                                                                                                                                                                                       RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS
                                                                                                                                                                                                                                                                                                                                                DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                                                                                                                                                                                                                                                                                                                                DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT 300
                                                                                                                                                                                                                                                                                                                                                                                                       MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
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Pred. No. 1.7e-268;
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RESULT 8

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                                                                                                                                                                                                                                                                                                                                 cc describes new Bacillus thuringlensis Cry3Bb mutant proteins, and comprovides methods for producing them. The B. thuringlensis Cry3Bb cc polypeptide was modified to have improved insecticidal activity or cenhanced insecticidal specificity against a target insect. The cc modification comprises at least one amino acid substitution, addition, corresponding to from about amino acids substitution occurs at a position cc corresponding to from about amino acids 1-365 of the unmodified cry3Bb cc polypeptide, wherein the substitution or deletion occurs at a position cc corresponding to from about amino acids 1-365 of the unmodified corresponding to from about amino acids 1-365 of the unmodified corresponding to from about amino acids 1-365 of the unmodified corresponding to from about amino acids 1-365 of the unmodified corresponding to from about amino acids 1-365 of the unmodified corresponding to from about amino acids 1-365 of the unmodified corresponding to from about amino acids 1-365 of the unmodified corresponding to from about amino acids 1-365 of the unmodified corresponding to from about amino acids 1-365 of the unmodified corresponding to from about amino acids 1-365 of the unmodified corresponding to from about amino acids 1-365 of the unmodified corresponding to from about amino acids 1-365 of the unmodified corresponding to from about amino acids 1-365 of the unmodified cry3Bb cry3Bb cry3Bb corresponding to from about amino acids 1-365 of the unmodified cry3Bb 
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18-DEC-1997;
18-DEC-1997;
18-DEC-1997;
                                                                                                                                                                                                                                                                                                                              Sequence
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121 IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 505-507; 512pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insecticidal Bacillus thuringiensis proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-395184/33.
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Romano C, S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cry3Bb; mutant; insecticidal activity; insecticidal specificity;
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                                                                                                                                                            1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS
                                             TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK
                                                                    TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
                                                                                                                                       MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS 68
                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                              652 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence of Cry3A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bryson JW, English L, atin SL, Von Tersch MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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97US-0993170.
97US-0993722.
97US-0993775.
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                                                                                                                                                                                                                               100.0%; Score 3406; DB 20; 100.0%; Pred. No. 1.7e-268; tive 0; Mismatches 0;
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Walters FS;
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RESULT 9
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ID AAA89960
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KW COLLER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus thuringiensis var. tenebrionis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis var. tenebrionis; insect resistance; transgenic plant; crop protection; crystal protein; toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-1996 (first entry)
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                        26-APR-1988;
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536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein - useful for Coleopteran insects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric plant gene which expresses a Bacillus thuringiensis protein - useful for prodn. of plants which are toxic to
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                                                                                                                                                                                             RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS
                 TENGSAATIYYTPDYSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
                                                                                                                                               KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
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                                                                                 MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
                                                                                                                               KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHELNYVMCFL
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TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
                                                               MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
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643; Conservative
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Pred. No. 2.9e-268;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                       Comparing the content and the CryIIIA protein standing scanning thurseness of domain II of the CryIIIA protein of Bacillus thurseness. All the positions changed to alanine in these proteins the located in some of the solvent exposed loops and beta-strands directed towards or located at the molecular appex. The substituted amino acids have a relative solvent accessibility of at least 40%, or are a commaximum distance of 3 amino acids away from an amino acid having at least Commaximum distance of 3 amino acids away from an amino acid having at least Commaximum distance of 3 amino acids away from an amino acid having at least Commaximum distance of 3 amino acids away from an amino acid having at least Commaximum distance of 3 amino acids away from an amino acid having at least Commaximum distance of 3 amino acids away from an amino acid having at least Commaximum distance of 3 amino acids away from an amino acid having at least Commaximum distance of 3 amino acids away from an amino acid having at least Commaximum distance of 3 amino acids away from an amino acid having at least Commaximum distance of 3 amino acids away from an amino acid having at least Commaximum distance of 3 amino acids away from an amino acid having at least Commaximum distance of 3 amino acids away from an amino acid having at least Commaximum distance of 3 amino acids away from an amino acid having at least Commaximum distance of 3 amino acids away from a mino acid having at least Commaximum distance of 3 amino acids away from a mino acid having at least Commaximum distance of 3 amino acids away from an amino acid having at least Commaximum distance of 3 amino acids away from an amino acid having at least Commaximum distance of 3 amino acids away from an amino acid having at least Commaximum distance of 3 amino acids away from an amino acid having at least Commaximum distance of 3 amino acids away from an amino acid and acids away from an amino acid and acids away from an amino acid acids away from an amino acid acids away from an amino aci
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                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
increased toxicity; Coleopteran insect; Colorado potato beetle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page -; 22pp; English.
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43; Conservative
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Pred. No. 2.9e-268;
1; Mismatches 0;
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                                               Novel Cryllia proteins AAW34811-41 were produced by alanine scanning mutagenesis of domain II of the Cryllia protein of Bacillus thurlengensis. All the positions changed to alanine in these proteins are located in some of the solvent exposed loops and beta-strands clarected towards or located at the molecular apex. The substituted amino acids have a relative solvent accessibility of at least 40%, or are a maximum distance of 3 amino acids away from an amino acid having at least 40% relative solvent accessibility. The novel Cryllia proteins have an increased toxicity to Coleopteran insects, e.g. Colorado potato beetle, cand can be used to combat, or improve plant resistance towards insects. Specifically, the toxicity of the present sequence towards Diabrotica confict virgifera was tested. The BC50 value (concentration at which to 50% feeding inhibition is observed) of the present protein was found to be 7.12 microgram per millilitre, compared to 4.04 microgram per content this sequence does not appear in the specification; it was created to information and appear in the specification; it was created content the present information and appear in the specification; it was created content to formation and appear in the specification; it was created content to formation and appear in the specification; it was created content to the present protein and the content of the present protein.
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increased toxicity; Coleopteran insect; Colorado potato beetle;
relative solvent_accessibility; plant resistance;
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CC Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning CC mutagenesis of domain II of the CryIIIA protein of Bacillus thuriengensis. All the positions changed to alanine in these proteins CC are located in some of the solvent exposed loops and beta-strands CC directed towards or located at the molecular apex. The substituted amino CC acids have a relative solvent accessibility of at least 40%, or are a CC maximum distance of 3 amino acids away from an amino acid having at least 10.0 relative solvent accessibility. The novel CryIIIA proteins have an increased toxicity to Coleopteran insects, e.g. Colorado potato beetle, CC and can be used to combat, or improve plant resistance towards insects. Specifically, the toxicity of the present sequence towards insects. CC virgifera virgifera was tested, and the present mutant protein was considered to be a "down mutant" for Diabrotica virgifera virgifera. The CC toxicity of the mutant protein for this blabrotica pest was significantly below the toxicity of the native CryIIIA protein.

CC note: this sequence does not appear in the specification; it was created considered the company of the mative CryIIIA protein.
Sequence
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644 AA;
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Query Match Best Local Matches al Similarity 643; Conserv Conservative 99.98; Mismatches Score 3403; DB 18; Pred. No. 2.9e-268; 1; Mismatches 0; Indels Length 644; 0 Gaps 60 0,

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toxicity; Coleopteran insect; Colorado potat
solvent accessibility; plant resistance;
a virgifera virgifera.
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                                                                                  cryIIIA gene; corn rootworm toxicity; Coincreased toxicity; Coleopteran insect; relative solvent accessibility; plant r
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                                     thuriengensis
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                                                                          virgifera virgifera.
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                                                                                    corn rootworm toxicity; CryIIIA protein;
icity; Coleopteran insect; Colorado potato beetle;
ent accessibility; plant resistance;
Location/Qualifiers
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                                       RDVLTDPIVGVNNLRGYGTTESNIENYIRKPHLEDYLHRIQEHTREQPGYYGNDSENYWS
                                                                                                                 DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                                                                                                                                      MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
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                                                                                                  DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                                                                                                                       MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
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643; Conserv
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/note= "wild type Val replaced with Ala"
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Pred. No. 3.5e-268;
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              YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
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                                                                                                                             MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC 540
YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN
                                                     TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
                                                                                                              MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
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Job time : Search completed: January 10, 2003, 11:06:28 41

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Scoring table:
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1,

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Listing first 45 summaries
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/laa/backfiles1.pep:*
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  US-08-996-441B-113
US-08-993-170A-113
US-08-993-170A-113
US-08-993-170B-113
US-08-993-75B-113
US-08-993-75B-113
US-08-995-43B-2
US-08-704-966-4
US-08-993-72A-109
US-08-993-72A-109
US-08-993-775B-109
US-08-993-775B-56
US-08-993-170A-109
US-08-993-170A-56
US-08-993-170A-56
US-08-993-170A-56
US-08-993-170A-50
US-08-993-170A-50
US-08-993-170A-50
US-08-993-170A-50
US-08-993-170A-50
US-08-993-170A-50
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US-08-072-281-2
US-08-095-060-2
US-08-295-446-2
US-09-027-998A-2
PCT-US92-11337-4
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Sequence 44, A	Sequence 44, A	•	•	•	•	Sequence 48, A	•	•	Sequence 48, A	•	•	•	•	•	•	•	•
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ALIGNMENTS

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US-07-828-788A-4
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US-07-828-788A-4
                                                                                                                                                                                                                                  TELEPHONE: 904-375-8100
TELEFAX: 904-372-8600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
TYPE: AMINO ACID
STRANDENMESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5273746
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/828
FILING DATE: 19200129
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-775-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PAYNE, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
               MOLECULE TYPE: Protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: NIGERIENSIS
INDIVIDUAL ISOLATE: PS40D1
IMMEDIATE SOURCE:
LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF FRANK GAERTNER
CLONE: 40D1
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CITY: GAINESVILLE
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2421 N.W. 41st STREET, SUITE
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APPLICANT: Fischhoff, David A.
APPLICANT: Euchs, Roy L.
APPLICANT: Lavrik, Paul B.
APPLICANT: McPherson, Sylvia A.
APPLICANT: Perlak, Frederick J.
TITLE OF INVENTION: Insect Resistant Plants
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                        Sequence 2, Applic Patent No. 5495071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                 CORRESPONDENCE ADDRESS
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                                                                                          ADDRESSEE: Lawrence M. Lavin, Jr., STREET: 700 Chesterfield Parkway N CITY: St. Louis STATE: Missouri
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7286
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUIENCE CHARACTERISTICS:
LENGTH: 644 amino acids
TYPE: AMINO ACID
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Matches
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CURRENT APPLICATION NUMBER: US/(
FILING DATE: 19930604
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
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FILING DATE: 14-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: LAVIN Jr., Lawrence
REGISTRATION NUMBER: 30,76
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              YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
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AMINO ACID
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
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REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-052
TELECOMMUNICATION INFORMATION:
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APPLICANT: JANSENS, Stefan
APPLICANT: PERFEROEN, Marn
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                    GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT 420
                                                                                                           GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT 420
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KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL 480
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P.O. Box 1404
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                                                                                                                                     ; MOLECULE TYPE: protein US-08-759-446-2
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                                                                                 Query Match 100.0%; Score 3406; DB 1; Best Local Similarity 100.0%; Pred. No. 7.1e-277;
                                                                      Matches 644;
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APPLICANT: Fischh
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (314) 537-7286 TELEFAX: (314) 537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 05-DEC-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                FILING DATE: 14-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lavin Jr., Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acid
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                                                                                                                                                                                                                                                                                                              NAME: Lavin Jr., Lawrence M.
REGISTRATION NUMBER: 30,768
REFERENCE/DOCKET NUMBER: 38-21(10629)A
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 63198
                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: St. Louis
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                  1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS 60
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MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS 60
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700 Chesterfield Parkway No.
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Perlak, Frederick J.
                                                                                                                                                                                                          644 amino acids
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Lavrik, Paul B.
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                                                                      Conservative
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                                                                      Mismatches
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                                                                                                   Length 644;
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US-09-027-998A-2
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GENERAL INFORMATION:
APPLICANT: Fischhoff, David A APPLICANT: Fuchs, Roy L APPLICANT: Perlak, Frederick J
           INFORMATION
                                                FILING DATE: 23-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Welinda L
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:195
                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Insect Resistant Plants
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White and Durkee
                                                                                                                                                                                                                                                          STREET:
CITY: HO
STATE: T
COUNTRY:
ZIP: 772
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                          TELEPHONE:
                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                Perlak, Frederick J
 (713) / (713) / (713) / (713)
                                                                                                                                                                            Release #1.0, Version
                                                                                                                                               US/09/027,998A
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                                                                                                                                    Sequence 4, Application PC/TUS9211337
GENERAL INFORMATION:
APPLICANT: PAYNE, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS
TITLE OF INVENTION: ACTIVE AGAINST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
COMPUTER READABLE FORM
                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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LENGTH: 644 amino acids
                 COUNTRY:
ZIP: 326
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TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
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                                             STREET: 2421 N.W. CITY: GAINESVILLE STATE: FL
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                                                                          ADDRESSEE: DAVID R. SAL
STREET: 2421 N.W. 41st
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                                                                                                                                                                                                                                                                                                                  YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
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                                                                                           SALIWANCHIK
                                                                            STREET,
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Pred. No. 7.1e-277;
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                                                                                                                                        THURINGIENSIS ISOLATES PHTHIRAPTERA PESTS
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Query Match
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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LIBRARY: LAMBO
CLONE: 40D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
                                                                                                                                                                                                                                                                                                     181 MPSFAISGYEVLELTTYAQAANTHLELLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS 180
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                     301
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481 MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PILING DATE: 19921231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
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                                                                                                                                                       GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWFSAVYSGVT 420
                                                                KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCEL 480
                                                                                                                                                                                                                                          RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLEDYLHRIQFHTREQPGYYGNDSFNYWS
                                                                                                                                                                                                                                                                                                                                                                                             MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
                                                                                                                                GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT
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                                           KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
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                                                                                                                                                                                    Matches 644;
                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,92
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                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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COUNTRY: US.
ZIP: 77210
121 IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS 180
                                                                                                                                                                                                                                                                                                    LENGTH:
TYPE: a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                   69 TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 128
                                                                                 61 TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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TELEFAX: 512/474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
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                                                                                                                                   1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS 60
                                                                                                                  9 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS
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P.O. Box 4433
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                                                                                                                                                                                    Conservative
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Von Tersch, Michael A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version
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                                                                                                                                                                                                100.0%; Score 3406; DB 3; Length 652; 100.0%; Pred. No. 7.2e-277;
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RESULT 8
US-08-993-722A-113
; Sequence 113, Application US/08993722A
Parent No. 6060594
                                  ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:149
                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                    APPLICATION NUMBER: US/08/993,722A FILING DATE: 18-DEC-1997 CLASSIFICATION: 435
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        IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS

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US-08-993-170A-113
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                                                                                                                                                                                 Patent No. 6063597
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Conserv
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                                                                                                                                                                          GENERAL INFORMATION:
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TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
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APPLICANT:
                                                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
           TITLE
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TOPOLOGY: 11
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           INVENTION:
R: Brussock, Sušan M.
R: Malvar, Thomas M.
R: Bryson, James W.
R: Kulesza, Caroline A.
R: Kulesza, Caroline A.
R: Walters, Frederick S.
R: Slatin, Stephen L.
R: Von Tersch, Michael A.
R: Von Tersch, Michael A.
R: INVENTION: POLYPEPTIDE COMPOSITIONS TOXIC TO
                                                                                                                                                     English, Leigh H.
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GENERAL INFORMATION:
APPLICANT: English
APPLICANT: Brussoc
APPLICANT: Malvar,
APPLICANT: Bryson,

Brussock, Susan M Malvar, Thomas M. Bryson, James W.

APPLICANT:

APPLICANT: APPLICANT: APPLICANT:

APPLICANT: Romano, Charles
TITLE OF INVENTION: NUCLEIC
TITLE OF INVENTION: COLEOP

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

ADDRESSEE:

E: Arnold, Wh

STREET: P.O. B CITY: Houston STATE: Texas

USA

TELECOMMUNICATION INFORMATION

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com)

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COLEOPTERAN INSECTS

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Best Local :
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REFERENCE/DOCKET NUMBER: MECO:002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEO ID NO: 113:
SEQUENCE CHARACTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 18-DEC-1997
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ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
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MGGSRGTIPVLTWTHKSVDEFNMIDSKKITQLPLVKAYKLQSGASVVAGPRETGGDIIQC
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                                                                                       KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL 480
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                                                                                                                                        GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT
                                                                     KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 113
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: TO: USA COUNTRY: USA 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: ME
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 TENGSAATIYVTPDVSYSQKYRARIHYASTSQITETLSLDGAPENQYYFDKTINKGDTLT 600
                               129
                                            121 IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 18 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
181 mpsfaisgyevlflttyaqaanthlfllkdaqiygeewgyekediaefykrqlkltqeyt 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                          69 TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWFSEDPWKAFMEQVEALMDQK 128
                                                                                                                        61 TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                         1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS 60
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                               IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
                                                                                                                                                                                                                       644;
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6077824
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Slatin, Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brussock, Susan
Malvar, Thomas M
Bryson, James W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kulesza, Caroline A. Walters, Frederick S.
                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                   Score 3406; DB 3; Pred. No. 7.2e-277;
                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                   Length 652;
                                                                                                                                                                                                                       Indels
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US-08-295-060-4
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US-08-295-060-4
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                                                                                                                                             INFORMATION FOR SEQ ID NO:
                              MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VAN RIE, Jeroen
APPLICANT: JANSENS, Stefan
APPLICANT: PERFEROEN, Marrix
TITLE OF INVENTION: NEW DIABROTICA TOXINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 645 amino acids
                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 01(
                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,060
FILING DATE: 26-AUG-1994
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Burns,
STREET: P.O. Box 1
CITY: Alexandria
STATE: Virginia
                                                                    TOPOLOGY:
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                                                                                  amino acid
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P.O. Box 1404
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                                                                                                                                                                                                                                              Patent No. 6013523
; GENERAL INFORMATION:
APPLICANT: Adang, Michael J.
APPLICANT: Rocheleau, Thomas A.
APPLICANT: Merlo, Donald
APPLICANT: Murray ""'
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US-08-704-966-2
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                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                         APPLICANT: Murray, Elizabeth E. TITLE OF INVENTION: Synthetic I TITLE OF INVENTION: Gene
                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         603 NSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                          COUNTRY: USA
ZIP: 32801
                                                                                                                               CITY: Orlando
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242
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                                                                                                              STATE:
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                                                                                                                                                                  ADDRESSEE:
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                                                                                                            Florida
                                                                                                                                             E: Saliwanchik, Lloyd & Saliwanchik
1000 Legion Place, Suite 1750
                                                                                                                                                                                                                       Gene
                                                                                                                                                                                                                                       Synthetic Insecticidal Crystal Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.7%;
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Pred. No. 2.4e-270;
0; Mismatches 9;
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US-08-704-966-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 407-839-8589
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATIÓN NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MP:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 407-426-7500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0: FILING DATE: 09-SEP-1988 ATTORNEY/AGENT INFORMATION: NAME: Lloyd, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 28-JAN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/369,839
FILING DATE: 06-JAN-1995
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                                                                                                                                                                                                                                                           348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168
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     481
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 MTADNNTEALDSSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MTADNNTEALDSSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWK 60
                                                                                                                                                                                                                                                                                                                                                                     ELFSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAE 227
                                                                                                                                                                                                                                           PGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTN 407
                                                                                                                                                                                                                                                                                                                    VRLYPKEVKTELTRDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLEDYLHRIQFHTRFQ
                                                                                              GYSHQLNYVMCFLMQGSRGTIFVLTWTHKSVDFFNMIDSKKITQLFLVKAYKLQSGASVV 527
AGPRETGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQY 587
                                                                           GYSHQLNYVMCFLMQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVV
                                                                                                                                                                                                                          PGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      597;
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100.0%; Pi
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GENERAL INFORMATION:
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                                                                                                                                              Matches
                                                                                                                                                                                Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rocheleau, Thomas A.
APPLICANT: Merlo, Donald
APPLICANT: Murray, Elizabeth E.
TITLE OF INVENTION: Synthetic I.
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 9
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.TELEPHONE: 407-426-7500
TELEFAX: 407-839-8589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/827,844
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/242,482
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: US 08/369,839
FILING DATE: 06-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 03-MAY-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 AFMEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 29-AU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik STREET: 1000 Legion Place, Suite 1750
                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/242,482 FILING DATE: 09-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30
61 AFMEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIR 120
                                                                                            48 MTADNNTEALDSSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWK 107
                                                                                                                                                             Local
                                                                                                                                                                                                                                                       TOPOLOGY: 11
                                                                       1 MTADNNTEALDSSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWK 60
                                                                                                                                              al Similarity
597; Conserv
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                                                                                                                                              Conservative
                                                                                                                                                                                                                                                         linear
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                                                                                                                                                             92.5%; Score 3149; DB 3; 100.0%; Pred. No. 2.1e-255;
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RESULT 14
US-08-704-966-4
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APPLICATION NUMBER: US 08/369,839
FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,191
FILING DATE: 03-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,844
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/242,482
FILING DATE: 09-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08704966 Patent No. 6013523 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Adang, Michael J.
APPLICANT: Rocheleau, Thomas A.
APPLICANT: Merlo, Donald
APPLICANT: Murray, Elizabeth E.
TITLE OF INVENTION: Synthetic Ins
                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                        APPLICATION NUMBER: US/08 FILING DATE: 29-AUG-1996 CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                      ADDRESSEE: Sal
STREET: 1000 L
CITY: Orlando
STATE: Florida
COUNTRY: USA
ZIP: 32801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRLYPKEVKTELTRDYLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYKRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYKRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYD 287
                                                                                                                                                                                                                                                                                                                                Florida
                                                                                                                                                                                                                                                                                                                                                        E: Saliwanchik, Lloyd & Saliwanchik
1000 Legion Place, Suite 1750
                                                                                                                                                                                                    US/08/704,966
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Sequence 4, Application US/08705438;
Patent No. 6015891
GENERAL INFORMATION:
APPLICANT: Adang, Michael J.
APPLICANT: Rocheleau, Thomas A.
APPLICANT: Murray, Elizabeth E.
APPLICANT: Murray, Elizabeth E.
                                                                                                    RESULT 15
US-08-705-438-4
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-704-966-4
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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 anino acids
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NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MPS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 407-426-7500
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                                                                                                                                                                                                                                                                                     GYSHQLNYVMCFLMQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVV
                                                                                                                                                                                                                                                                                                                                       LAVWPSAVYSGYTKVEFSOYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEK
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Pred. No. 5.8e-255;
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APPLICANT: MUITAY, Elizabeth E. TITLE OF INVENTION: Synthetic I TITLE OF INVENTION: Gene NUMBER OF SEQUENCES: 9

Synthetic Insecticidal Crystal Protein Gene 9

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; LENGTH: 610 amino acid
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-705-438-4
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Best Local Similarity 99.8%;
Matches 596; Conservative
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MPS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 407-426-7500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/705,438
FILING DATE: 29-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/369,839
FILING DATE: 06-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 28-JAN-1 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/057,191
FILING DATE: 03-MAY-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/827,844 FILING DATE: 28-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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LAVWPSAVYSGVTKVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEK 467
                                FYKRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYD
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                                                                                                                                                                                                                                                                                                                          AFMEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIR 120
                                                                                                                                                                                                                                                                                                                                               AFMEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIR 167
                                                                                                                                                                              FYKRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLTALFPLYD
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1000 Legion Place, Suite 1750
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09-SEP-1988
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Pred. No. 5.8e-255;
0; Mismatches 1;
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                                                                                                                                    GYSHQLNYVMCFLMQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVV 527
                                                         AGPRETGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITETLSLDGAPENQY 540
                                                                           AGPRETGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQY 587
                                                                                                                     GYSHQLNYVMCFLMQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVV 480
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Job time : 18 secs Search completed: January 10, 2003, 11:08:25

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OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_AA: *
                                                                                                                                       : /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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SUMMARIES

1 2 3 3 3 5 5 6 6 8 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
3406 1214.5 1214.5 1214.5 1195.5 1194.5 1194.5 1194.5 1194.5 1194.5 1195.5 1103.5 11095.5	Score
100.0 35.7 35.7 35.3 35.1 35.1 35.1 35.1 35.1 35.1 35.2 32.2 32.2 32.2 32.2 32.2	Query
644 667 673 1210 673 673 669 669 670 670 670 670 620 620 620 620 621	Length
	BB
US-10-943-692-2 US-10-032-717-8 US-10-032-717-18 US-10-032-717-12 US-10-032-717-12 US-10-032-717-16 US-10-032-717-16 US-10-032-717-40 US-10-032-717-44 US-10-032-717-24 US-10-032-717-30 US-10-032-717-30 US-10-032-717-32 US-10-032-717-32 US-10-032-717-32 US-10-032-717-32 US-10-032-717-32 US-10-032-717-32 US-10-032-717-32 US-10-032-717-32	ID
Sequence 2, Appli Sequence 8, Appli Sequence 4, Appli Sequence 4, Appli Sequence 12, Appl Sequence 2, Appl Sequence 6, Appli Sequence 10, Appl Sequence 11, Appl Sequence 2, Appli Sequence 2, Appli Sequence 44, Appl Sequence 24, Appl Sequence 30, Appl Sequence 30, Appl Sequence 31, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 42, Appl Sequence 42, Appl Sequence 46, Appl Sequence 46, Appl Sequence 46, Appl	Description

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301.7 209.7 208.6 208.5	31.2
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US-09-826-660-27 US-09-756-543-2 US-09-756-643-2 US-09-873-873-28 US-09-873-873-12 US-09-873-873-12 US-09-873-873-12 US-09-873-873-12 US-09-873-873-14 US-09-873-873-30 US-09-873-660-6 US-10-120-544A-4 US-09-873-756-754A-20 US-09-873-756-754A-20 US-09-873-756-754A-20 US-09-873-756-754A-20 US-09-756-754A-20 US-09-756-754A-8 US-10-120-544A-8 US-10-120-544A-8 US-10-120-544A-8 US-10-120-544A-8	US-09-826-660-25
10, April 10, Ap	Sequence 25, Appl

ALIGNMENTS

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RESULT 1
US-09-943-692-2
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; Patent No. US20020152496A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LAVRIK, PAUL B.
APPLICANT: MCPHERSON, SYLVIM A.
APPLICANT: MCPHERSON, SYLVIM A.
APPLICANT: PERLAK, FREDERICK J.
APPLICANT: PERLAK, FREDERICK J.
TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
FILE REFERENCE: MOBT:195-1
CURRENT APPLICATION NUMBER: US/09/943,692
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/027,998
PRIOR APPLICATION NUMBER: 09/027,998
PRIOR TILING DATE: 1998-02-23
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: FISCHHOFF, DAVID A.
APPLICANT: FUCHS, ROY L.
                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 3406; DB 10; Length 644; Best Local Similarity 100.0%; Pred. No. 3e-258; Matches 644; Conservative 0; Mismatches 0; Indels 0;
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
121 IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS 180
                             121 IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS 180
                                                                                                      61 TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
                                                                                                                              61 TTKDVIQKGISVVGDLLGVVGEPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
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; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (truncated)
US-10-032-717-8
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                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/10032717 Patent No. US20020151709A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lynn E. Sims
TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Prot.
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. I
APPLICANT: Xiang Feng
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115 ALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNDHSQGRIRELESQAE 174
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                                                      61 EVLVSGQDAAKAAIDIVGKLLSGLGVPFVGPIVSLYTQLIDILWPSGQKSQWEIFMEQVE 120
                                                                                         61 ----TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPS--EDPWKAFMEQVE 114
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                                                                                                                             1 MSPNNQNEYEIIDATPSTSVSNDSNRYPFANEPTNALQNMDYKDYLKMSAGNASEYPGSP 60
                                                                                                                                                              1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS 60
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                                                                                                                                                                                                                 268;
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Theodore W. Kahn
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                     35.7%; Score 1214.5; DB 12; Length 667; 39.0%; Pred. No. 5.3e-87; tive 134; Mismatches 222; Indels 63;
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US-10-032-717-18
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                                                                                                                                                                                                                SEQ ID NO 18
LENGTH: 673
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Ronald D. Flanna
                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 200 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/242,838
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With TITLE OF INVENTION: Pesticidal Activity Against Coleopterans FILE REFERENCE: 35718/237005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Theodore W. APPLICANT: Lynn E. Sims
                                                                                                                                                                                         ORGANISM: Bacillus thuringiensis (truncated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          622 ----IGVTGLSAGDKVYIDKIEFIPVN 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                532 SDLAPSITGGPNNTVVSGPGFTGGGIIKVIRNGVIISHMRVKISDINKEYSMRIRYASAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518 YKLQSGA-----SVVAGPRETGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 VKTELTRDVLTDPIVGVNNLRGYGT-----TFSNIE-NYIRKPHLFDYLHRIQFHTR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 LTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ELINQKIAEYARNKALSELEGLGNNYQLYLTALEEWKENPNGSR----ALRDYRNRFEILD
                                                                                                               Local Similarity
1 MSPNNQNEYEIIDATPSTSVSNDSNRYPFANEPTNALQNMDYKDYLKMSAGNASEYPGSP 60
                                     1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETTDEPLEKGYSHQLNYVMCFLMQGS-RGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKA 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTNL---AVWP---SAVYSGVTKVEFSQYNDQTDEASTQTYDS-KRNVGAVSWDSIDQLPP 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SISSARY----IRHWAGHQISYH-RIFSDNIIKQMYGTNQNLHSTSTFDFTNYDIYKTLS 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETSDQPNYESYSHRLCHITSIPATGSTTGLVPVFSWTHRSADLINAVHSDKITQIPVVKV 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDAVLLDIVFPGYTYIFFGMPEVEFFMVNQLNNTRKTLKYNPVSKDIIAGTRDSELELPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ronald D. Flannagan
Theodore W. Kahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/10032717
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                     2000-10-24
                                                                                                    35.7%; Score 1214.5; DB 12; Length 673; 39.0%; Pred. No. 5.4e-87;
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US-10-032-717-4
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                                                          ; LENGTH: 1210
TYPE: PRT
ORGANIZM: Bacillus thuringiensis
US-10-032-717-4
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APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. I
APPLICANT: Xiang Feng
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                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
Query Match
Best Local Similarity
                                                                                                                                               SEQ ID NO 4
                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/242,838 PRIOR FILING DATE: 2000-10-24 NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                             APPLICANT: Lynn E. S1ms
TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
CURRENT FILING DATE: 2001-10-23
                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0
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Ronald D. Flannagan
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35.7%;
Score 1214.5; DB pred. No. 1.3e-86;
                     DB 12;
                     Length 1210;
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NUMBER OF SEQ ID NOS: 48
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 673
                                                                                   APPLICANT: Lynn E. Sims
IIILE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                  APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xlang Feng
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Theodore W. Kahn
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                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                 Sequence 22, Application US/10032717 Patent No. US20020151709A1
                                 APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Xiang Feng
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Sins
TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
EILE REFERENCE: 35718/237005
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               CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE:
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PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 22
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TYPE: PRT
ORGANISM: Bacillus thuringlensis (mutated)
                                                                              648 PNSTLSGI-----VYVDRIEFIPVD 667
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                                                                                                                                                      ADI--VLHVNDA---QIQMPKTMNPGEDLTSKTFKVADAITTLNLATDSSLALKHNLGED
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Sequence 6, Application US/10032717
Patent No. US20020151709A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Micholas B. Duck
APPLICANT: Miang Feng
APPLICANT: Ronald D. Flannagan

APPLICANT:

Theodore W. Kahn Xiang Feng Ronald D. Flannagan

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US-10-032-717-10
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 6
LENGTH: 667
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Best Local Similarity
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Sequence 10, Application US/10032717 Patent No. US20020151709A1
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TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR ETLING DATE: 2000-10-24
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                                                                                                                                     645 NSTLSGI-----VYVDRIEFIPVD
                                                                                                                                                                             621 QIGVTGLSAGDKVYIDKIEFIPVN 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -FQPGYYGNDSFNYWSGNYVS-TRPSIGSNDIITSPFYG-NKSSEPVQNLEFNGEKVYRA 402
                                                                                                                                                                                                                          DI--VLHVNDA---QIQMPKTMNPGEDLTSKTFKVADAITTLNLATDSSLALKHNLGEDP
                                                                                                                                                                                                                                                                                                                 KCWDNLPFVPVVKGPGHTGGDLLQYNRSTGSVGTLFLARYGLALEKAGKYRVRLRYATDA
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                                                                                                                                                                                                                                                                       QITFTLSLDGAPFNQYYFDKTINKGDTLTYNSFNLASFSTPFELS-----GNNL 620
                                                                                                                                                                                                                                                                                                                                                           KAYKLQSGASVVAGPRFTGGDIIQCTEN-GSAATIYVTP---DVSYSQKYRARIHYASTS 571
                                                                                                                                                                                                                                                                                                                                                                                                          PPETSDQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAV
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38.9%; Pred. No. 2e-85;
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Best Local Similarity
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TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REPERENCE 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
PRIOR FILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Nicholas B.
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELINQKIAEYARNKALSELEGLGNNYQLYLTALEEWEENPNGSR----ALRDVRNRFEILD 177
DI--VLHVNDA---QIQMPKTMNPGEDLTSKTFKVADAITTLNLATDSSLALKHNLGEDP 644
                                                                                                                                KAYKLQSGASVVAGPRFTGGDIIQCTEN-GSAATIYVTP---DVSYSQKYRARIHYASTS 571
                                                                                                                                                                                                                                                                                                                                                    SISSARY----IRHWAGHQISYHRVSRGSN---LQQMYGTNQNLHSTSTFDFTNYDIYKT 409
                                           QITETLSLDGAPFNQYYFDKTINKGDTLTYNSFNLASFSTPFELS-----GNNL 620
                                                                                     KCWDNLPFVPVVKGPGHTGGDLLQYNRSTGSVGTLFLARYGLALEKAGKYRVRLRYATDA 589
                                                                                                                                                                                                                                                               LSKDAVLLDIVYPGYTYIFFGMPEVEFFMVNQLNNTRKTLKYNPVSKDIIASTRDSELEL
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Theodore W. Kahn
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APPLICANT: Nicholas B. Du
APPLICANT: Xiang Feng
APPLICANT: Ronald D. Flan
APPLICANT: Theodore W. Ka
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SEQ ID NO 16
LENCTH: 669
TYPE: PRT
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Best Local
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TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/242,838 PRIOR FILING DATE: 2000-10-24 NUMBER OF SEQ ID NOS: 48
530 KCWDNLPFYPYYKGPGHTGGDLLQYNRSTGSYGTLFLARYGLALEKAGKYRYRLRYATDA 589
                                            516 KAYKLQSGASVVAGPRFTGGDIIQCTEN-GSAATIYVTP---DVSYSQKYRARIHYASTS 571
                                                                                             470 PPETSDQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAV
                                                                                                                                         457 PPETTDEPLEKGYSHQLNYVMCFLMQG-SRGTIPVLTWTHKSVDFFNMIDSKKITQLPLV 515
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                                                                                                                                                                                       LSKDAVLLDIVYPGYTYIFFGMPEVEFFMVNQLNNTRKTLKYNPVSKDIIASTRDSELEL 469
                                                                                                                                                                                                                                                                                  SISSARY----IRHWAGHQISYHRVSRGSN----LQQMYGTNQNLHSTSTFDFTNYDIYKT 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTGEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFFLYDVRLYFKE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELINQKIAEYARNKALSELEGLGNNYQLYLTALEEWEENPNGSR---ALRDVRNRFEILD 177
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                                                                                                                                                                                                                                                                                                                              -FQPGYYGNDSENYWSGNYVS-TRPSIGSNDIITSPFYG-NKSSEPVQNLEFNGEKVYRA 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTAEYSDHCVKWYETGLAKLKGTSAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPME
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Ronald D. Flannagan
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CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
PRIOR SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 673
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TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
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APPLICANT: Nicholas B. 1
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456 LPPETTDEPLEKGYSHQLNYVMCFLMQG-SRGTIPVLTWTHKSVDFFNMIDSKKITQLPL 514
                                           413 TLSKDAVLLDIVYPGYTYIFFGMPEVEFFMVNQLNNTRKTLKYNPVSKDIIASTRDSELE
                                                                                   402 AVANTNL---AVWP--SAVYSGYTKVEFSQYNDQTDEASTQTYDS-KRNVGAVSWDSIDQ 455
                                                                                                                                 360 RSISSARY----IRHWAGHQISYHRVSRGSN---LQQMYGTNQNLHSTSTFDFTNYDIYK
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Cald D. Flannagan
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Theodore W. Kahn
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APPLICANT:
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TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR APPLICATION NUMBER: 50/242,838
PRIOR SEQ ID NOS: 48
NUMBER OF SEQ ID NOS: 48
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                    EVLVSGQDAAKAAIDIVGKLLSGLGVPFVGPIVSLYTQLIDILWPSGEKSQWEIFMEQVE 120
                                                                                                                                                       SHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLK 234
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                         -FQPGYYGNDSFNYWSGNYVS-TRPSIGSNDIITSPFYG-NKSSEPVQNLEFNGEKVYRA 402
                                                                                                     VKTELTRDVLTDPIVGVNNLRGYGT-----TFSNIE-NYIRKPHLFDYLHRIQFHTR--
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  SISSARY----IRHWAGHQISYHRVSRGSN---LQQMYGTNQNLHSTSTFDFTNYDIYKT 409
                                                                              TKAQLTREVYTDPL-GAVNVSSIGSWYDKAPSFGVIESSVIRPPHVFDYITGLTVYTQSR 356
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44
LENGTH: 670
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APPLICANT: Lynn E. Sins
APPLICANT: Lynn E. Sins
TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: 05/10/032,717
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
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APPLICANT: Nicholas B. I
APPLICANT: Xiang Feng
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                                                                                                                                                                                                                                                 115 ALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAE 174 | ::|| | : :| | : :| | : :| | : :|
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                                                                                                                                                           SHFRNSMPSFAISGYEVLFLITYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLK 234
                                                                                                                                                                                                                        LTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFFLYDVRLYPKE 294
    VKTELTRDVLTDPIVGVNNLRGYGT-----TFSNIE-NYIRKPHLFDYLHRIQFHTR--
                                              LTAEYSDHCVKWYETGLAKLKGTSAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPME 298
                                                                                                                                    SLFTQYMPSFRVTNFEVPFLTVYAMAANLHLLLLKDASIFGEEWGWSTTTINNYYDRQMK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.0%; Score 1192; DB 12; ilarity 38.7%; Pred. No. 3.1e-85; Conservative 134; Mismatches 225;
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; LENGTH: 670
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-10-032-717-24
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Patent No. US20020151709A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With TITLE OF INVENTION: Pesticidal Activity Against Coleopterans ETLE REFERENCE: 35718/237005 CURRENT APPLICATION NUMBER: US/10/032,717 CURRENT FILING DATE: 2001-10-23 PRIOR APPLICATION NUMBER: 60/242,838 PRIOR APPLICATION NUMBER: 60/242,838 PRIOR FILING DATE: 2000-10-24 NUMBER OF SEQ ID NOS: 48
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             179
                      175 SHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLK 234
                                                                               121 ELINQKIAEYARNKALSELEGLGNNYQLYLTALEEWEENPL--KMSRALRDVRNRFEILD 178
                                                                                                                          115 ALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAE 174
                                                                                                                                                                    61 EVLVSGQDAAKAAIDIVGKLLSGLGVPFVGPIVSLYTQLIDILWPSGEKSQWEIFMEQVE 120
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Local Similarity 38.6%; Pred. No. 5.3e-85;
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                                                                                                                                                                                                                                                                                              1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS 60
SLFTQYMPSFRVTNFEVPFLTVYAMAANLHLLLLKDASIFGEEWGWSTTTINNYYDRQMK 238
                                                                                                                                                                                                                                                      MSPNNQNEYEIIDATPSTSVSNDSNRYPFANEPTNALQNMDYKDYLKMSAGNASEYPGSP 60
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Theodore W. Kahn
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US-10-032-717-30
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APPLICANT: Nicholas B. Du
APPLICANT: Xiang Feng
APPLICANT: Ronald D. Flan
APPLICANT: Theodore W. Ka
APPLICANT: Lynn E. Sims
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 620
TYPE: PRT
                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lynn E. Sims
TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT ENCIRCATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
CURRENT FILING DATE: 2001-10-23
CURRENT FILING DATE: 2001-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/242,838 PRIOR FILING DATE: 2000-10-24
103 -EDPWKAFMEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPH 161
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                                                               1 MSAGNASEYPGSPEVLVSGQDAAKAAIDIVGKLLSGLGVPFVGPIVSLYTQLIDILWPSG 60
                                                                                                           MTADNNTEALDSS----TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPS- 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SISSARY----IRHWAGHQISYHRVSRGSN----LQQMYGTNQNLHSTSTFDFTNYDIYKT 410
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Ronald D. Flannagan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Theodore W. Kahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicholas B. Duck
                                                                                                                                                                   Conservative 117;
                                                                                                                                                                                    32.4%; Score 1103.5; DB 12; Length 620; 39.5%; Pred. No. 2.3e-78;
                                                                                                                                                              Mismatches 210; Indels 59;
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162

SQGR-IRELFSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGY 220

EKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNNYQLYLTALEEWEENPNGSRNGS

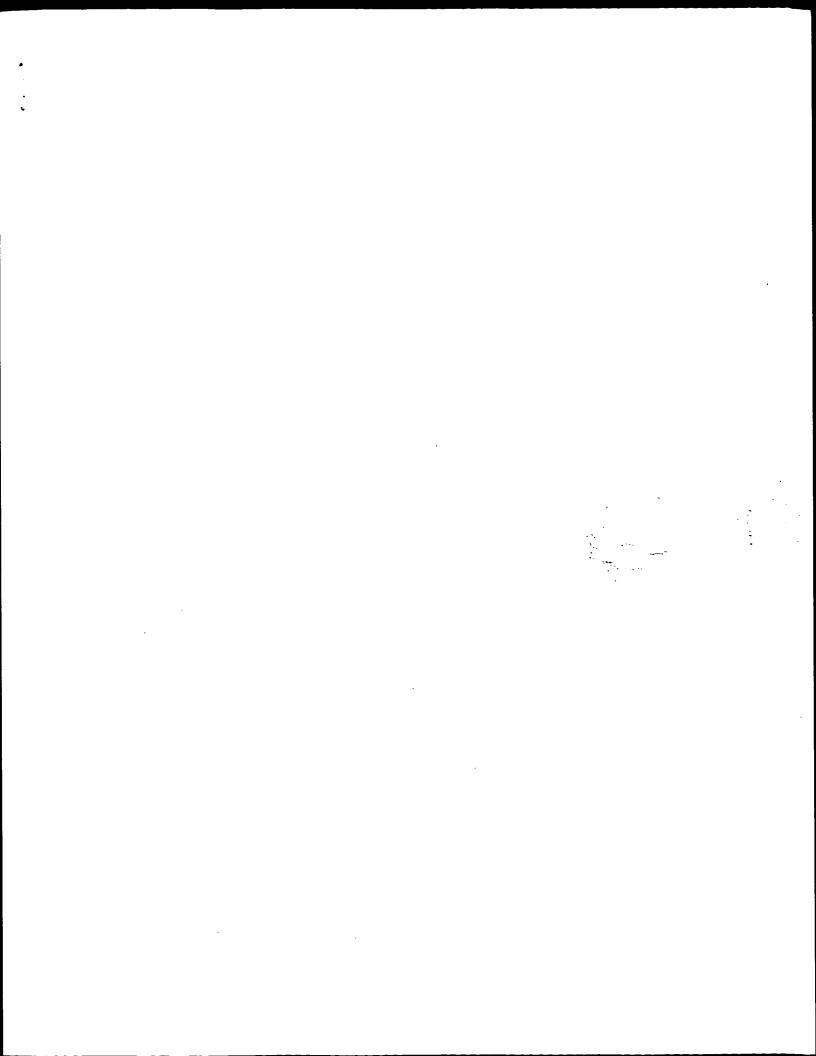
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US-10-032-717-32
Sequence 32, Application U:
Patent No. US20020151709A1

; ORGANISM: Bacillus thuringiensis (mutated)
US-10-032-717-32

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Xiang Feng
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Sims
TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
PRIOR PPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                          LENGTH: 62
TYPE: PRT
473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389 VQNLEFNGEKVYRAVANTNL---AVWP--SAVYSGVTKVEFSQYNDQTDEASTQTYDS-K 442
                                                                                       \vdash
                                                                                                                         MTADNNTEALDSS----TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPS- 102
                                                                                  MSAGNASEYPGSPEVLVSGQDAAKAAIDIVGKLLSGLGVPFVGPIVSLYTQLIDILWPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFLMQG-SRGTIPVLTWTHKSVDFF 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSTFDFTNYDIYKTLSKDAVLLDIVYPGYTYIFFGMPEVEFFMVNQLNNTRKTLKYNPVS 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALFPLYDVRLYPKEVKTELTRDVLTDPIVGVNNLRGYGT-----TESNIE-NYIRKPHL 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STTTINNYYDROMKLTAEYSDHCVKWYETGLAKLKGTSAKOWVDYNOFRREMTLAVLDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGKYRVRLRYATDADI -- VLHVNDA -- - QIQMPKTMNPGEDLTSKTFKVADAITTLNLAT 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQCTEN-GSAATIYVTP---DVSY 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDIIASTRDSELELPPETSDOPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLN 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKEDIAEFYKROLKLTOEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLI 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDYITGLTVYTQSRSISSARY----IRHWAGHQISYHRVSRGSN---LQQMYGTNQNLHS 352
                                                                                                                                                                     250;
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                                                                                                                                                               32.2%; Score 1096.5; DB 12; Length 620; illarity 39.2%; Pred. No. 7.9e-78; Conservative 118; Mismatches 211; Indels 59;
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588 DSSLALKHNLGEDPNSTLSGI-----VYVDRIEFIPVD
                                                                                        533 AGKYRVRLRYATDADI--VLHVNDA---QIQMPKTMNPGEDLTSKTFKVADAITTLNLAT 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RALRDVRNRFEILDSLFTQYMPSERVTNFEVPELTVYAMAANLHLLLLKDASIFGEEWGW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQGR-IRELFSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGY 220
                                                                                                                                                                               NTIYSDKITQIPAVKCWDNLPFVPVVKGPGHTGGDLLQYNRSTGSVGTLFLARYGLALEK 532
                                                                                                                                                                                                                              NMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQCTEN-GSAATIYVTP---DVSY 557
                                                                                                                                                                                                                                                                                                                                                                        TSTEDETNYDIYKTLSKDAVLLDIVYPGYTYIFFGMPEVEFFMVNQLNNTRKTLKYNPVS 412
                                                                                                                                                                                                                                                                                                                                                                                                                       VQNLEFNGEKVYRAVANTNL---AVWP--SAVYSGVTKVEFSQYNDQTDEASTQTYDS-K 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDYITGLTVYTQSRSISSARY----IRHWAGHQISYHRVSRGSN---LQQMYGTNQNLHS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDYLHRIQFHTR---FQPGYYGNDSFNYWSGNYVS-TRPSIGSNDIITSPFYG-NKSSEP 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALFPLYDVRLYPKEVKTELTRDVLTDPIVGVNNLRGYGT----TFSNIE-NYIRKPHL 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKEDIAEFYKROLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREWTLTVLDLI 280
                                            ------GNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
                                                                                                                                     SQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLTYNSFNLASFSTPFELS- 616
                                                                                                                                                                                                                                                                               KDIIASTRDSELELPPETSDQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLN 472
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Search completed: January 10, 2003, 11:08:43 Job time: 13 secs



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OM protein - protein search, using sw model
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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3406
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Post-processing: Minimum Match 08 Listing first 45 summaries Maximum Match 100%

Database PIR_73:*
1: pir1:
2: pir2: pir1:*
pir2:*
pir3:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	_	NO.	Result
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1166	823	1176	1189	1176	1176	1176	655	1176	934	1155	1155	1181	1156	1155	1155	1154	1160	1228	719	719	1157	1138	719	719	659	652	649	652	Length	
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parasporal crystal	parasporal crystal	parasporal crystal	parasporal crystal	hypothetical prote	parasporal crystal											

ALIGNMENTS

A;Cross-references: GB:M22472; NID:g142733; PIDN:AAA22336.1; PID:g142734
A;Experimental source: strain San Diego
R;Hoefte, H.; Seurinck, J.; Van Houtven, A.; Vaeck, M.
Nucleic Acids Res. 15, 7183, 1987
A;Title: Nucleotide sequence of a gene encoding an insecticidal protein of Bacillus t A;Reference number: A26853; MUID:88015559; PMID:3658680
A;Accession: A26853 Gene 57, 37-46, 1987

A; Title: Nucleotide sequence and deduced amino acid sequence of a coleopteran-active A; Reference number: A27323; MUID:88112860; PMID:2828180 C;Species: Bacillus thuringiensis C;Date: 19 Nov-1988 #sequence-vision 19-Nov-1988 #text_change 01-Dec-2000 C;Accession: A7323; A26853; A29987; A28407; S60781; I39812; I39813 R;Herrnstadt, C.; Gilroy, T.E.; Sobieski, D.A.; Bennett, B.D.; Gaertner, F.H. parasporal crystal protein cry3Aal - Bacillus thuringiensis N;Alternate names: coleopteran-specific insect control protein; crystal protein cryC; A; Molecule type: DNA A; Residues: 1-652 <HER> A; Accession: A27323

A; Molecule type: DNA A; Residues: 9-652 <HOE>

A;Cross-references: GB:Y00420; NID:g40252; PIDN:CAA68482.1; PID:g40253
A;Experimental source: var. tenebrionis
R;McPherson, S.A.; Perlak, F.J.; Fuchs, R.L.; Marrone, P.G.; Lavrik, P.B.; Fischhoff, Bio/Technology 6, 61-66, 1988
Bio/Technology 6, 61-66, 1988
A;Title: Characterization of the coleopteran-specific protein gene of Bacillus thurin A;Reference number: A29987
A;Accession: A29987

A; Molecule type:

DNA

A; Experimental source: var. tenebrionis
R; Sekar, V.; Thompson, D.V.; Maroney, M.J.; Bookland, R.G.; Adang, M.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 7036-7040, 1987 A; Residues: 9-652 <MCP>

A;Title: Molecular cloning and characterization of the A;Reference number: A28407 A;Accession: A28407 insecticidal crystal protein

A; Molecule type: DNA A; Residues: 9-652 <SEK>

R;Adams, L.F.; Mathewes, S.; O'Hara, P.; Petersen, A.; Guertler, H.
Mol. Microbiol. 14, 381-389, 1994
A;Title: Elucidation of the mechanism of CryIIIA overproduction in a mutagenized stra
A;Reference number: S60781; MUID:95131759; PMID:7830581
A;Accession: S60781

A; Status: nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA A; Residues: 9-652 < ADA>

A;Cross-references: EMBL:U10985; NID:g506182; PIDN:AAC43266.1; PID:g514312 A;Experimental source: var. tenebrionis strain NB176, a mutant of strain NB125 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1 1994

YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 652

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C;Keywords: delta-endotoxin
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R;Telxelra De Souza, M.; Lecadet, M.M.; Lereclus, D.
J. Bacteriol. 175, 2952-2960, 1993
A;Title: Full expression of the cryIIIA toxin gene of Bacillus thuringiensis requires
A;Reference number: 139813; MUID:93259939; PMID:8491716
A;Accession: 139813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RiDonovan, W.P.; Gonzalez, J.M.
Mol. Gen. Genet. 214, 365-372, 1988
Mol. Gen. Genet. 214, 365-372, 1988
A;Title: Isolation and characterization of EG2158, a new strain of Bacillus thuringiens;
A;Reference number: I39812; MUID:89112139; PMID:3146015
A;Accession: I39812
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A; Residues: 9-58 < RE2>
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A;Residues: 9-652 <RES>
A;Cross-references: GB:M37207; NID:g142735; PIDN:AAA50255.1; PID:g142736
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TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
                                                              MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
                                                                                MGGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
                                                                                                                                            KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
                                                                                                                                                                                                         GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWDSAVYSGVT 420
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Similarity 100.0%;
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A;Gene: cryIIID C;Superfamily: parasporal crystal protein
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A;Accession: JH0261
A;Molecule type: DNA
A;Residues: 1-649 <LAM>
A;Residues: 1-649 <LAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
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                                                                                   539 DIIKCT-NGSGLTLYVTPAPDLTYSKTYKIRIRYASTSQVRFGIDLGSYTHSISYFDKTM
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DKGNTLTYNSFNLSSVSRPIEISGGNKIGVSVGGIGSGDEVYIDKIEFIPMD
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74.4%; Pred. No. 4.3e-161;
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parasporal crystal protein cry3Bb1 - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cryIIIB2
C:Species: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 01-Dec-2000
C;Accession: I39811
RESULT 4
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parasporal crystal parasporal cryst
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C; Super:
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A;Molecule type: DNA
A;Residues: 1-652 <RES>
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A;Title: Characterization of two genes encoding Bacillus thuringlensis
A;Reference number: 139811; MUID:93119147; PMID:1476436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CFLMQDRRGTIPFFTWTHRSVDFFNTIDAEKITQLPVVKAYALSSGASIIEGPGFTGGNL
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                                                                                                                                                                                                           DDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSNEKIYIDKIEFIPV
                                                                                                                                                                                                                                                                            GDTLTYNSFNLASFSTPFELSG--NNLQIGVTGLSAGDKVYIDKIEFIPV 643
                                                                                                                                                                                                                                                                                                                                                   LFLKESSNSIAKFKVTLNSAALLQRYRVRIRYASTTNLRLFVQNSNNDFLVIYINKTMNK
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   protein cry3Ba1 - Bacillus thuringiensis (fragment)
coleopteran-active parasporal crystal protein; delta-endotoxin
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Pred. No. 2.1e-146;
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C:Species: Bacillus thuringiensis
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Dec-2000
C:Accession: S10228
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Nucleic Acids Res. 18, 1305, 1990
A;Title: Nucleotide sequence of a coleopteran-active toxin
A;Reference number: $10228; MUID:90206811; PMID:2320431
A;Accession: $10228
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C;Superfamily: parasporal crystal
C;Keywords: delta-endotoxin; toxir
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A;Molecule type: DNA
A;Residues: 1-659 <SIC>
A;Cross-references: EMBL:X17123; NID:g40258;
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                                                                                                                                                                                                                                          VTKVEFSQYNDQTDEASTQTYDSKRNVGAV-SWDSIDQLPPETTDEPLEKGYSHQLNYVM 477
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                                                                                                          IQCTE-NGSAATIYVT-PDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINK 595
                                                                                                                                               CFLMQDRRGTIPFFTWTHRSVDFFNTIDAEKITQLPVVKAYALSSGASIIEGPGFTGGNL
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DGDLTYQTFDFATSNSNMGFSGDTNDFIIGAESFVSNEKIYIDKIEFIPV
                                  GDTLTYNSFNLASFSTPFELSG--NNLQIGVTGLSAGDKVYIDKIEFIPV 643
                                                                       LFLKESSNSIAKFKVTLNSAALLQRYRVRIRYASTTNLRLFVQNSNNDFLVIYINKTMNI 608
                                                                                                                                                                                                                    VTKVDFSQYDDQKNETSTQTYDSKRYNGYLGAQDSIDQLPPETTDEPLEKAYSHQLNYAE
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Pred. No. 3.8e-144;
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cryV465 protein - Bacillus thuringlensis
C;Species: Bacillus thuringlensis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 26-Aug-1999
C;Accession: I40590
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.

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RESULT 6
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                     Insecticidal protein cryv - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change
C;Accession: I39815
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A; Residues: 1-719 <RES>
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A;Title: Distribution of cryv-type insecticidal protein genes in Bacillus thuringiensis
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     A.P.;
                                                                                                                                                                              PVPV
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                                                                                                                                                                                                                                             KAINQGNFSATMNRGEDLDYKTFRTIGFTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIE
                                                                                                                                                                                                                                                                       APFNQYYFDKTINKGDTLTYNSFNLASFSTPFELSG--NNLQIGVTGLSAGDKVYIDKIE 639
                                                                                                                                                                                                                                                                                                                      SGAAVVRGPGFTGGDILRRTNTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSING
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                                                                                                                                                                                                                                                                                                                                                                                                GQPNYESYSHRLSHI--GLISASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLS 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESLAGLNLFLTQPVNGVPRVDFHWKFPTLPIASDNFYYLGYAGVGTQLQDSENELPPETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -TRFQPGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRA 402
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R.; Hedges,
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C;Superfamily: parasporal crystal protein
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A;Molecule type: DNA
A;Residues: 1-719 <RES>
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C;Genetics:
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A;Accession: I39815
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A;Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes
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640 FVPV 643
                                   640 FIPV 643
                                                                     580 KAINQGNFSATMNRGEDLDYKTFRTVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIE
                                                                                                        582 APFNQYYFDKTINKGDTLTYNSFNLASFSTPFELSG--NNLQIGVTGLSAGDKVYIDKIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 LMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAES 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 FVSAST---IQTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEE
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                                                                                                                                                                            SGASVVAGPRFTGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDG
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                                                                                                                                                SGAAVVRGPGFTGGDILRRTNTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSING
                                                                                                                                                                                                                                  GQPNYESYSHRLSHI---GLISASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLS
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parasporal crystal protein cry7Aal - Bacillus thuringiensis W;Alternate names: parasporal crystal protein cryIIIC C:Species: Bacillus thuringiensis C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_chc:Accession: A48944

#sequence_revision 18-Nov-1994 #text_change

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A48944 RESULT 7 Ş

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A;Status: preliminary
A;Molecule: type: DNA; protein
A;Residuele: 1-1138 <LAM>
A;Residuele: 1-1138 <LAM>
A;Cross-references: GB:M64478; NID:g142760; PIDN:AAA22351.1; PID:g142761
A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBIP:112093)
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C; Keywords: delta-endotoxin
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A;Title: Novel Bacillus thuringiensis insecticidal crystal protein with a silent activit A;Reference number: A48944; MUID:92384571; PMID:1514800
A;Contents: BTS137J
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parasporal crystal protein cry9Cal [validated] - Bacillus thuringiensis N;Alternate names: parasporal crystal protein cryIH C;Species: Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Species: O1-Dec-2000 #sequence_revision O1-Dec-2000 #text_change O1-Dec-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NT--AINTVVSVTGATLSALGVPGASFITNFYLKIAGLLWPENGKIWDEFMTEVEALIDQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDP-WKAFMEQVEALMDQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNLNNLDGYE-----DSNRTLNNSLNYPTQKALSPSLKNMNYQDFLSITEREQPEALASG 55
                                                                                                                                                                                            SNNSSFYVDSIEFIPVD
                                                                                                                                                                                                                                                                                         GQFNVYINDKITLQTKFQNTVETIGEGKDLTYGSFGYIEYSTTIQFPDEHPKITLHLSDL
                                                                                                                                                                                                                                                                                                                                      APFNOYYFDK-----TINKGDTLTYNSFNLASFSTPFELSGNN--LQIGVTGL 627
                                                                                                                                                                                                                                                                                                                                                                                      DPSTVVKGPGFTGGDLVKRGSTGYIGDIKATVNSPLSQKYRVRVRYATNV-----S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TQLTREVYTDPVSLSISN-PDIGPSFSQMENTAIRTPHLVDYLDELYIYTSKYKAFSHEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEFSMPSFKVTGYEIPLLTVYAQAANLHLALLRDSTLYGDKWGFTQNNIEENYNRQKKRI 227
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                                                                                                                                                                                                                                            SAGDKYYIDKIEFIPVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        parasporal crystal protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YWSAHKVSFKKSEQSN-LYTTGIYG-KTSGYISSGAYSFHGNDIYRTLA
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R;Lambert, B.; Buysse, L.; Decock, C.; Jansens, S.; Piens, C.; Saey, B.; Seurinck, J. Appl. Environ. Microbiol. 62, 80-86, 1996
A;Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity a A;Reference number: A59350; MUID:96141404; PMID:8572715
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A; Residues: 1-1157 <LAM>
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631 QEILTVNAEGVSTGGEYYIDRIEIVPVN 658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKTELTRDVLTDDIV-----GVNNLRGYGT----TFSNIEN-YIRKPHLFDYLHRIQFHT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTAKYTNYCETWYNTGLDRLRGTNTESWLRYHQFRREWTLVVLDVVALFPYYDVRLYPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDFVNAIPLFAVNGQQVPLLSVYAQAVNLHLLLLKDASLFGEGWGFTQGEISTYYDRQLE
                                            N--LQIGVTGLSAGDKVYIDKIEFIPVN 644
                                                                                           VRFASTGNFSIRVLRGGVSIGDVRLGSTMNRGQELTYESFFTREFTTTGPFNPPFTFTQA
                                                                                                                                                                                         TPNRITQLPLVKASAPVSGTTVLKGPGFTGGGILRRTTNGTFGTLRVTVNSPLTQQYRLR
                                                                                                                                                                                                                                      DSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQCTENGSAATIYVTPDVSYSQKYRAR
                                                                                                                                                                                                                                                                                       NDELPPDESTGSS-----THRLSHVTFFSFQTNQAGSIANAGSVPTYVWTRRDVDLNNTI
                                                                                                                                                                                                                                                                                                                                  IDQLPP-ETTDEPLEKGYSHQLNYVMCFLMQ------GSRGTIPVLTWTHKSVDFFNMI 504
                                                                                                                                                                                                                                                                                                                                                                                 AVDFRSALI-----GIY-GVNRASFVPGGLFNGTTSPANGGCRD------LYDT
                                                                                                                                                                                                                                                                                                                                                                                                                             GEKVYRAVANTNIAVWPSAVYSGVTKVEF---SQYNDQTDEASTQTYDSKRNVGAVSWDS 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRFP--VSSNFMDYWSGH--TLRRSYLNDSAVQEDSYGLITTTRATINPGVDGTNRIEST 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RFQPGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYG-----NKSSEPVQNLEFN 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNPQLTREVYTDPIVFNPPANVGLCRRWGTNPYNTFSELENAFIRPPHLFDRLNSLTISS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELVNQQITEFARNQALARLQGLGDSFNVYQRSLQNWLADRNDTRN---LSVVRAQFIALD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLSISGRDAVQTALTVVGRILGALGVPFSGQIVSFYQFLLNTLWPVNDTAIWEAFMRQVE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --SSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDP--WKAFMEQVE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNRNNQNEYEIIDAPHCGCPSDDDVRYPLASDPNAALQNMNYKDYLQMTDEDYTDSYINP 60
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1.9e-67;
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parasporal crystal protein crylial - Bacillus thuringiensis N;Alternate names: delta-endotoxin; parasporal crystal protein cryV C;Species: Bacillus thuringiensis C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 01-Dec-2000

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insecticidal protein cryV1 - Bacillus thuringiensis
C;Speckes: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
C;Accession: I39814
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C; Superfamily
C; Keywords: d
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R;Tailor, R; Tippett, J; Gibb, G; Pells, S; Pike, D; Jordan, L; Ely, S. Mol. Microbiol. 6, 1211-1217, 1992
A;Title: Identification and characterization of a novel Bacillus thuringiensis A;Reference number: S25383; MUID:92269582; PMID:1588820
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A; Residues: 1-719 < TAI>
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 FVSAST---IQTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
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                                                                                                                                                                                      FIPV 643
                                                                                                                                                                                                                 KAINQGNFSATMNRGEDLDYKTFRTVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIE
                                                                                                                                                                                                                                                    APFNQYYFDKTINKGDTLTYNSFNLASFSTPFELSG--NNLQIGVTGLSAGDKVYIDKIE 639
                                                                                                                                                                                                                                                                                                                             SGASVVAGPRFTGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDG 581
                                                                                                                                                                                                                                                                                                                                                                GQPNYESYSHRLSHI--GLISASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLS
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                                                                                                                                                                                                                                                                                            SGAAVVRGPGFTGGDILRRTNTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKLKNQDKHQSFSSNAKVDKISTDSLK-----NETDIELQNINHEDCLKMSEYENVEP 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251;
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A;Gene: cryV1
C;Superfamily: parasporal crystal protein
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A;Title: Distribution of cryV-type insecticidal protein genes in tomocidus.
A;Reference number: I39814; MUID:95314293; PMID:7793960
A;Accession: I39814
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Cross-references: GB:L36338; NID:g540281; PIDN:AAC36999.1; PID:
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Best Local
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640 FVPV
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                                                                                                                                 SGAAVVRGPGFTGGDILRRTNTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSING
                                                                                                                                                                                                                                                                                                                                                                                   -TRFQPGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRA 402
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37.8%;
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Pred. No. 1.2e-67;
2; Mismatches 239;
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RESULT 11 S00873

parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis N;Alternate names: parasporal crystal protein cryA4 C;Species: Bacillus thuringiensis subsp. thuringiensis C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Dec-2000

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A; Molecule type: DNA
A; Residues: 1-1228 <BRI>
A; Cross-references: EMBL:)
C; Genetics:
A; Gene: cryA4
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C;Superfamily: parasporal c:
C;Keywords: delta-endotoxin
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R;Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus A;Reference number: S00873; MUID:88203216; PMID:3362680
A;Accession: S00873
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parasporal crystal protein cry8Cal - Bacillus thuringiensis N;Alternate names: parasporal crystal protein cryIII C;Species: Bacillus thuringiensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTELTRDVLTDPI--VGVN--NLRGYGT---TFSNIE-NYIRKPHLFDYLHRIQFHTRFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HFRNSMPSFAISGYEVLELTTYAQAANTHLELLKDAQIYGEEWGYEKEDIAEFYKRQLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QITENARNTALARLQGLGDSFRAYQQSLEDWLEN----RDDARTRSVLYTQYIALEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRE-LFSQ---AES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTSNRKNENEIINAVSNHSAQMD-------LLPDARIEDSLCIAEGNNIDPFVSA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNLAVWPSAVY----SGVTKVEFSQYNDQ--TDEAS---TQTYDSKRNVGAVSWDSIDQL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRWSNTRHMTYWRGHTIQSRP-IGGG--LNTSTHGATNTSINPV-TLRFASRDVYRTESY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSA-S 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFLNAMPLFAIRNQEVPLLMYYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVER 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGVLLW--GIYLEPIHGVPTVRFNFTNPQNISDRGTANYSQPYESP---GLQLKDSETEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYG--NKSSEPVQNLEFNGEKVYRAVAN 405
                                                                                                                                                                     IDKIEFIPV 643
                                                                                                                                                                                                                             VSRGGTTVNNFRFLRTMNSGDELKYGNFVRRAFTTPFTFTQTQDIIRTSIQGLSGNGEVY 626
                                                                                                                                                                                                                                                LSLDGAPENQYYEDKTINKGDTLTYNSENLASESTPEELS--GNNLQIGVTGLSAGDKVY 634
                                                                                                                                                                                                                                                                                                                                                   AYKLQSGASVVAGPRFTGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFT 576
                                                                                                                                                                                                                                                                                                                                                                                                                              PPETTDEPLEKGYSHQLNYVMCFLMQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVK 516
                                                                                                                                                IDKIEIIPV 635
                                                                                                                                                                                                                                                                                                               ASELPQGTTVVRGPGFTGGDILRRTNTGGFGPIRVTVNGPLTQRYRIGFRYASTVDFDFF
                                                                                                                                                                                                                                                                                                                                                                                            PPETTERPNYESYSHRLSHIGIILQ--SRVNVPVYSWTHRSADRTNTIGPNRITQIPMVK
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RESULT 13 S39536

parasporal crystal protein cry9Bal - Bacillus thuringiensis
N;Alternate names: delta-endotoxin-related protein; parasporal crystal prot
C;Species: Bacillus thuringiensis
C;Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000

parasporal crystal protein

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R;Sato, R.; Takeuchi, K.; Ogiwara, K.; Minami, M.; Kaji, Y.; Suzuki, N.; Hori, H.; As Curr. Microbiol. 28, 15-19, 1994
A;Title: Cloning, heterologous expression, and localization of a novel crystal protei A;Reference number: I40589; MUID:94100786; PMID:7764305
A;Accession: I40589
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A;Cross-references: EMBL:U04366; NID:g532523; PIDN:AAA21119.1; PID:g532524
C;Superfamily: parasporal crystal protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 YTARYSDHCVQWYNAGLNKLRGTGAKQWVDYNRFRREMNVMVLDLVALFPNYDARIYPLE
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623 PINLGISGSSRTFDISITKEAGAANLYIDRIEFIPVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALMDOKIADYAKNKALAELOGLONNVEDYVSALSSWOKNPVSSRNPHSOGRIRELFSQAE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKTELTRDVLTDPIVGVNNLRGYGTT------FSNIENYIRKPHLFDYLHRI 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RMYTSFRQNGTIEYY-----NYWGGQRLTLSYIYGSSFNKYSGVLAGAEDIIPVGQN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AILRINMGSFSQINYETPLLPTYAQAASLHLLVMRDVQIYGKEWGYPQNDIDLFYKEQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELIDQKILDSVRSRAIADLANSRIAVEYYQNALEDWRKNPHSTR---SAALVKERFGNAE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TT----KDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPS--EDPWKAFMEQVE 114
                                            PFEL----SGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
                                                                                                                                                                                          NFIYATKISQIPINKASRTSGGAVWNFQEG-LYNGGPVMKLSGSGSQVINLRVATDAKGA
                                                                                                                                                                                                                               NMIDSKKITQLPLVKAYKLQSGA--SVVAGPRFTGGDIIQCTENGS-AATIYVTPDV-SY 557
                                                                                                                                                                                                                                                                                 GIKTIDSGEELTYEN----YQSYSHRVSYITSFEIKSTGGTVLGVVPIFGWTHSSASRN 505
                                                                                                                                                                                                                                                                                                                              GAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFLMQGSRGT----IPVLTWTHKSVDFF 501
                                                                                                                                                                                                                                                                                                                                                                                ---DIYRVVWTYIGRYTNSLLGVNPVTFY-----FSNNTQ----KTYSKPKQFAG
                                                                                                                                                                                                                                                                                                                                                                                                                            NGEKVYRAV-----ANTNLAVWPSAVYSGVTKVEFSQYNDQTDEASTQTYDSKRNV--
                                                                                                                                        SQKYRARIHYASTSQITETLSLDGAPEN-----QYYFDKTINKGDTLTYNSFNLASFST 611
                                                                                            SQRYRIRIRYASDRAGKFTIS-SRSPENPATYSASIAYTNTMSTNASLTYSTFAYAE-SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247;
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R;Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H. Gene 53, 113-119, 1987
A;Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis A;Reference number: A26513; MUID:87248103; PMID:3297927
                                                                                                                            C;Species: Bacillus thuringiensis
C;Date: 11-Mar-1988 #sequence_revision 11-Mar-1988 #text_change 01-Dec-2000
                                                                                                                                                                      parasporal crystal protein - Bacillus thuringiensis (strain aizawai)
C; Species: Bacillus thuringiensis
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A; Accession: A26513
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A;Molecule type: DNA
A;Residues: 1-1154 <SH
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R:Shevelev, A.B.; Svarinsky, M.A.; Karasin, A.I.; Kogan, Y.N.; Chestukhina, G.G.; St FEBS Lett. 336, 79-82, 1993
A;Title: Primary structure of the cryX, the novel delta-endotoxin-related gene from A;Reference number: S39536; MUID:94085596; PMID:8262221
A:Accession: S39536.
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A; Cross-references: EMBL: x75019
                                                                                                                    Accession: A26513
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                                                                                                                                                                                                                                                                                                                                                         TYNSFNLASFSTPFELSGNNLQIGV--TGLSAGDKVYIDKIEFIPVN 644
                                                                                                                                                                                                                                                                                                          RYESFATREFTTDFNFRQPQELISVFANAFSAGQEVYFDRIEIIPVN 654
                                                                                                                                                                                                                                                                                                                                                                                                             RTGVGTFGTIRVRTTAPLTQRYRIRERFASTTNLFIGIRVGDRQVNYFDFGRTMNRGDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GINIYSGNLPTYVWTHRDVDLTNTITADRITQLPLVKSFEIPAGTTVVRGPGFTGGDILR
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSR----GTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRETGGDIIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NALTCEQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL----MQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAV-WPSAVYSGVTKVEF------SQY 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRRNYGSTTS-IVNYFSFNDRDYYQINTRSHTGLGFQNAPLFGITRAQFYPGGTYSVTQR 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMTESNLENATISSPHLEDTINNLMIYTGSESVHLTNQLIEGWIGHSVTSSLLASGPTTV 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --TFSNIEN-YIRKPHLEDYLHRIQFHTREQPGYYGNDSFNYWSGNYVSTRPSIGSNDII 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATLMAMDLIALFPYYNTRRYPIAVNPQLTREVYTDPL-GVPSEESSLFPELRCLRWQETS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTLIVLDLIALEPLYDVRLYPKEVKTELTRDVLTDPIVGVNN------LRGYGT- 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KYGARWGLRESQIGNLYFNELQTRTRDYTNHCVNAYNNGLAGLRGTSAESWLKYHQFRRE 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IYGEEWGYEKEDIAEFYKRQLKL-TQEYTDHCYKWYNVGLDKLRGSSYESWVNFNRYRRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -NGVRANLVLQRFEILHALFVSSMPSFG-SGPGSQRFQAQLLVVYAQAANLHLLLLLADAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNPHSQGRIRELFSQAESHFRNSMPSFAISG----YEVLFLTTYAQAANTHLFLLKDAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPSEDP--WKAFMEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYKDYLKMSEGDYIDSYINPGNVRTGLQTGIDIVAVVVGALGGPVGGILTGFLSTLFGFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NYKEFLRMTADNNTEA-LDSSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTI 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPSNDQAVWEAFIEQMEELIEQRISDQVVRTALDDLTGIQNYYNQYLIALKEWEERP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 117; Mismatches 237; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Svarinsky, M.A.; Karasin, A.I.; Kogan, Y.N.; Chestukhina, G.G.; Stepa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.0%; score 988; DB 2; Length 1154; 35.4%; Pred. No. 7.7e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----NYNSIDELPSLDPNEPISRSYSHRLSHITSYLHRVLTID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bac
                                 parasporal crystal protein crylAb3 - Bacillus thuringiensis
N;Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic
C;Species: Bacillus thuringiensis
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 01-Dec-2000
C;Accession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD0002
R;Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.
Agric. Biol. Chem. 51, 455-463, 1987
A;Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxi
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닭 δÃ 밁

A; Reference number: A90025 A; Accession: A90025 A; Molecule type: mRNA

of two insecticidal delta-endotoxin

genes

crystal

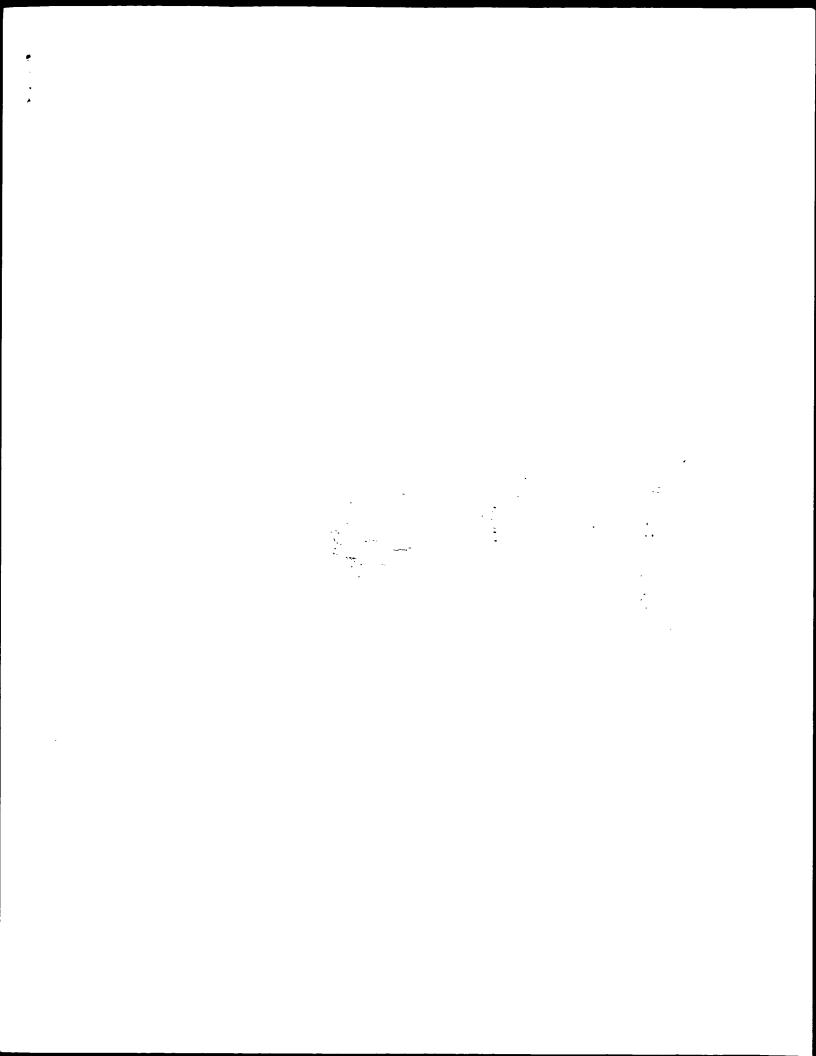
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RESULT 15
JD0002
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-115 <OED>
A;Cross-references: GB:M16463; NID:g143098; PIDN:AAA22551.1; PID:g143099
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                        603
                                                                                                                                                                                                                                           584 FNOYYFDKTINKGDTLTYNGFNLASFSTPFELSGNNLQIGVTGLSA-----GDKVYIDKI 638
                                                                                                                                                                                                                                                                                                  486 TSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRP
                                                                                                                                                                                                                                                                                                                                                                   524
                                                                                                                                                                                                                                                                                                                                                                                                       469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 FNIGINNQQLSYL-DGTEFA----YGTSSNLPSAYYRKSGTYDSLDEIPPQNNNYPPRQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415 VYSGVTKVEFSQYNDQTDEASTQTYDSKRNVGAVSW-----DSIDQLPPETTDEPLEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357 NYWSGNYVSTRPSIGSNDIITSPFYGNK-SSEPVQNLEFN-GEKVYRAVANTNLAVWPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 DQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 TQFLLSEFVPGAGFVLGLV-------DIIWGIFGPSQ--WDAFLVQIEQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 TKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIW----PSEDPWKAFMEQVEALM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 NPN------INECIPYNCLS-----NPEVEVLGGE---RIETGYTPIDISLSL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                      EFIP 642
                                                                                                                                                                                                                                                                                                                                                   ASVVAGPRETGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAP
                                                                                                                                                                                               INQGNFSATMSSGSNLQSGSFRTVGFTTPFNFSNGS---SVFTLSAHVFNSGNEVYIDRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                        YSHQLNYVMCFLMQGSRGTI-----PVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNSMPSFAISGYEVLFLITTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -YWSGHQIMASPYGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST---LYRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLTREIYTNPV--LENFDGSFRALAQGIEGSIRSPHLMDILNSITIYTDAHRGEY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELTRDVLTDPIVGVNNLRG-YGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 980; DB 2;
Pred. No. 2.6e-56;
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                                                                                                                                                                                                                                                                                                                                                      583
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C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
F;82-586/Product: toxic peptide #status predicted <TXP>
F;82-300/Region: toxic #status predicted
F;300-586/Region: insecticidal #status predicted
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A;Residues: 1-1155 <CHA>
A;Residues: 1-1155 <CHA>
A;Cross-references: EMBL:x54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
A;Cross-references: EMBL:x54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
A;Hofte, H.; de Greve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekercl Eur. J. Biochem. 161, 273-280, 1986
Eur. J. Biochem. 161, 273-280, 1986
A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thu: A;Reference number: A26461; MUID:87054026; PMID:3023091
A;Accession: A26461
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A;Cross-references: GB:M15271; NID:g143123; PIDN:AAA22561.1; A;Experimental source: subsp. kurstaki
R;Wablko, H; Raymond, K.C.; Bulla Jr., L.A.
DNA 5, 305-314, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-730,'L',732-784,'R',786-1155 <HOF>
A; Residues: 1-730,'L',732-784,'R',786-1155 <HOF>
A; Cross-references: GB:X04698; NID:940254; PIDN:CAA28405.1; PID:940255
A; Experimental source: strain berliner 1715
C; Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
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A;Cross-references: GB:M13898; NID:g142719; PIDN:AAA22330.1;
A;Experimental source: subsp. berliner
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A;Experimental source: subsp. kurstaki
A;Experimental source: subsp. kurstaki
R;Gelser, M.; Schweitzer, S.; Grimm, C.
Gene 48, 109-118, 1986
A;Title: The hypervariable region in the genes coding for entomopathogenic crystal prote
A;Reference number: A91560; MUID:87163505; PMID:3557124
A;Accession: A91560
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                                 298
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ELTRDYLTDPIVGVNNLRG-YGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSF 356
                                                                                         NYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVS
                                                                                                                             EYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKT
                                                                                                                                                                                                                   TTAIPLEAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIG 201
                                                                                                                                                                                                                                                                                  RNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TQFLLSEFVPGAGFVLGLV--------DIIWGIFGPSQ--WDAFLVQIEQLI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPN-----INECIPYNCLS-----NPEVEVLGGE---RIETGYTPIDISLSL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.8%; Score 980; DB 2; Length 1155; ilarity 33.9%; Pred. No. 2.6e-56; Conservative 124; Mismatches 231; Indels 8
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[6] SEQUENCE FROM N.A.

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EMBL; J00278; AAA222541.1; -.
EMBL; M37207; AAA50255.1; -.
EMBL; U10985; AAC43266.1; -.
EMBL; M30503; AAA2336.1; ALT_
PIR; A26853; A26853.
                                                                                                                                                                                                                                                                                       CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00555; endotoxin;
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MEDLINE=92049729; PubMed=1658659;
181 MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thuringiensis at 2.5-A resolution.";
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MEDLINE-88112860; PubMed-2828180;
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                                               IADYAKNKALAELOGLQNNVEDYVSALSSWOKNPVSSRNDHSQGRIRELFSQAESHFRNS
                                                                                                                                                                          MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS
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MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
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BEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
                                                                                                             TTKDVIOKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
                              IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
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A27323; A27323.
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644 AA;
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57 REMOVED IN MATURE FORM.
644 PESTICIDIAL CRYSTAL PROTEIN CRY3AA
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein cry3Ca (Insecticidal delta-endotoxin cry1IC(a)) (Crystaline entomocidal protoxin) (73 kDa crystal
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                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Bacteria; Firmicutes; Bacillales; Bacillaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      active crystal protein from strain subsp. kurstaki.";
Gene 110:131-132(1992).
                                                                                                                                                                                                                                                            -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lambert B., Theunis W., Aguda R., Van Audenhove K., Decock C., Jansens S., Seurinck J., Peferoen M.; "Nucleotide sequence of gene cryllID encoding a novel coleopte active crystal protein from strain BTI109P of Bacillus thuring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92184108; PubMed=1544571;
                                                                                                                                                                                                                                                                                                                                                                                      EUNCTION: PROFESSION OF COLEOPTERA.

EPITHELIAL CELLS OF COLEOPTERA.

DEVELOPMENTAL STACE: THE CRYSTAL PROTEIN

TS ACCUMULATED BOTH AS AN
                                                                                                                                                                                                                                                                                                                                        MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a novel coleopteran-
Bacillus thuringiensis
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Best Local
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                                                                                            C3BB_BACTU STANDARD; PRT; 652 AA.

Q06117; Q45717;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry3Bb (Insecticidal delta-endotoxin
Cry1IIB(b)) (Crystaline entomocidal protoxin) (74 kDa crystal
                                                CRY3BB OR CRYIIIB(B) OR CRYIIIB2.
Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales;
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   STRAIN-EG4961;
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                                    NCBI_TaxID=1428;
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             SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                        GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWP-----SAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTKDAIQKGISIIGDLLGVVGFPYGGALVSFYTNLLNTIWPGEDPLKAFMQQVEALIDQK
                                                                                                                                                                                                                                                    NKGDTLTYNSFNLASFSTPFELS-GNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
                                                                                                                                                                                                                                                                                         HSGYTKVQFSQYNDRKDEVRTQTYDSKRNVGGIVFDSIDQLPPITTDESLEKAYSHQLNY
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                                                                                                                                                                                                                              DKGNTLTYNSFNLSSVSRPIEISGGNKIGVSVGGIGSGDEVYIDKIEFIPMD
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                                                   Bacillales;
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                                                   Bacillaceae;
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                                                   Bacillus
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MEDLINE-93119147; PubMed=1476436;
Donovan W.P., Rupar M.J., Slaney A.C., Malvar T., Gawron-Burke Donovan W.P., Rupar M.J., Slaney A.C., Malvar T., Gawron-Burke Donovan W.P., Rupar M.J., Slaney A.C., Malvar T., Gawron-Burke Donovan W.P., Gawron-Burke T., Gawron-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Donovan W.P., Rupar M.J., Slaney
"Bacillus thuringiensis cryIIIC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent number US5378625, 03-JAN-1995.
-I- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS EPITHELIAL CELLS OF COLEOPTERA. HAS MODI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M89794; AAA22334.1; -. EMBL; U31633; AAA74198.1; -. HSSP; P07130; 1DLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insects.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOUTHERN CORN ROOTWORM. SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TERMINUS
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OF TOXICITY TO
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Pfam; PF00555; endotoxin; 1.
         Local
             Similarity
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289
352
417
451
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 Conservative
                                                                                                                                                                     endotoxin;
                                                        21
97
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419
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          68.7%;
                                             74385 MW;
                                                     Q -> P (IN STRAIN EG5144).

N -> D (IN STRAIN EG5144).

I -> V (IN STRAIN EG5144).

F -> S (IN STRAIN EG5144).

YYL -> IYF (IN STRAIN EG5144).

S -> G (IN STRAIN EG5144).

L -> I (IN STRAIN EG5144).

K -> I (IN STRAIN EG5144).

K -> I (IN STRAIN EG5144).
75; Mismatches
             Score 2341.5; DB 1; Length 652; Pred. No. 1.4e-146;
                                             63048332CDE8CCC6 CRC64;
  Indels
  7;
  Gaps
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120

60 60

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KIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRN 179 TVKDAVGTGISVVGQILGVVGVPFAGALTSFYQSFLNTIWPSDADPWKAFMAQVEVLIDK 1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRWTADNNTEALDSS

61

Qy 밁

180 121 120

S 문 Ş 밁

TDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTEL

SMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEY KIEEYAKSKALAELQGLQNNFEDYVNALNSWKKTPLSLRSKRSQDRIRELFSQAESHFRN

SMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWGYSSEDVAEFYHRQLKLTQQY

240 239

TDHCVNWYNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFYDIRLYSKGVKTEL

241 240 181 Š

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Query Match Best Local

DB 1;

Length

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RESULT 4
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ID C3BA_B
AC P17969
DT 01-NOV
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                                                                                                                                       EMBL; X17123; CAA34983.1; -. EMBL; A07234; CAA00645.1; -. PIR; S10228; S10228.
                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90206811; PubMed-2320431;
Sick A., Gaertner F.H., Wong A.;
"Nucleotide sequence of a coleopteran-active toxin gene from a new isolate of Bacillus thuringlensis subsp. tolworthi.";
Nucleic Acids Res. 18:1305-1305(1990).
-I- FUNCTION: PROMOTES COLLODOSMOTIC LYSIS BY BINDING TO THE MIDGUT
                                                      InterPro; IPR001178; Endotoxin. Pfam; PF00555; endotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
30-MAY-2090 (Rel. 39, Last annotation update)
Pesticidial crystal protein cry3Ba (Insecticidal d
CrysIIB(a)) (Crystaline entomocidal protoxin) (75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein).
CRY3BA OR CRYIIIB(A) OR CRYIIIB.
CRY3BA OR CRYIIIB(A) OR CRYIIIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus thuringiensis (subsp. tol
Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C3BA_BACTO
P17969;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPITHELIAL CELLS OF COLEOPTERA.

DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
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                                                                                                                        P07130; 1DLC
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                                    Sporulation.
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   75159 MW;
5A5B214FF84168CA CRC64;
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16-OCT-2001 (
16-OCT-2001 (
Pesticidial (
                                                                                                                                                                                                                                                                                                     C8AA_BACUK
Q45704;
                          STRAIN-NRIL B-18746 / PS50C;
Payne J.M., Sick A.J., Foncerrada L.;
"Novel coleopteran-active Bacillus thuringlensis isolate
gene encoding a coleopteran-active toxin.";
Patent number EP0498537, 12-AUG-1992.
-I- FUNCTION: PROMOTES COLLOHOOSMOTIC LYSIS BY BINDING TO
                                                                                                                                                                                                                      16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry8Aa (Insecticidal delta-endotoxiocryvIIIA(a)) (Crystaline entomocidal protoxin) (131 kDa crystal
                                                                                                                                                               Bacillus thuringiensis (subsp. kumamotoensis).
Bactaria; Firmicutes; Bacillales; Bacillaceae;
    - 1 - DEVELOPMENTAL STAGE: THE
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                  protein
                                                                                                                                                        NCBI_TaxID=132267;
                                                                                                                                                                                                CRY8AA OR CRYVIIIA(A).
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                  EPITHELIAL CELLS OF COLEOPTERA
                                                                                                                                                                                                                                                                                                                                                                                          DGDLTYQTFDFATSNSNMGFSGDTNDFIIGAESFVSNEKIYIDKIEFIPV
                                                                                                                                                                                                                                                                                                                                                                                                                    GDTLTYNSFNLASFSTPFELSG--NNLQIGVTGLSAGDKVYIDKIEFIPV 643
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                                                                                                                                                                                                                                                                                                                     STANDARD;
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CRYSTAL PROTEIN
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Pred. No. 2.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAQLTRDVYTDPIAFNIVTSTGFCNPWSTHSGILFYEVENNVIRPPHLFDILSSVEINTS 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAEYSDYCVKWYKIGLDKLKGTTSKSWLNYHQFRREMTLLVLDLVALFPNYDTHMYPIET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               004364; AAA21117.1; -. P07130; IDLC.
              LLSMGDFSSGQEVYIDRIEFIPVD
                                                                                                                                 ARIHYASTSQITETLSLDGAPENQYYFDKTINKGDTLTYNSFNLASESTPFEL--SGNNL 620
                                                                                                                                                                                                                     MIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQCTENGSAATIYVTPDVSYSQKYR 562
                                                                                                                                                                                                                                                                                                                                                                               VANLANYYQKAYGVPGS----WFHMVKRGTSSTTAYLYSKTHTALQGCTQVYESS----
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                                                       QIGVTGLSAGDKVYIDKIEFIPVN 644
                                                                                                                                                                                                                                                                                   -----DEIPLDRT-VPVAESYSHRLSHITSHSFSKNGSAYYGSFPVFVWTHTSADLNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRIRYASTTDFEFTLYL-GDTIEKNRFNKTMDNGASLTYETFKFASFITDFQFRETQDKI 638
                                                                                                                                                                                               TIYSDKITQIPAVKGDMLYLGGSVVQGPGFTGGDILKRTNPSILGTFAVTVNGSLSQRYR
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40.2%; Pred. No. 8.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry8Ba (Insecticidal delta-endotoxin CryVIIIB(a)) (Crystaline entomocidal protoxin) (134 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C8BA_BACUK
Q45705;
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CRYBBA OR CRYVIIIB(A) OR 50C(B).
CRYBBA OR CRYVIIIB(A) OR 50C(B).
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Bacteria; Firmicutes; Bacillales; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U04365; AAA21118.1; -. HSSP; P07130; 1DLC.
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                                  VKTELTRDVLTDPI--VGVNNLRGY---GTTFSNIEN-YIRKPHLFDYLHRIQFHTRFQP
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                                                                                                                                                                                                                                                                                                SHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPS--EDPWKAFMEQVE 114
TTAQLTREVYTDPLGAVDVPNIGSWYDKAPSFSEIEKAAIRPPHVFDYITGLTVYTK-KR
                                                                                                                     LTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKE
                                                                                                                                                                                                                                                                                                                                                               ELINQKIAEYARNKALSELEGLGNNYQLYLTALEEWKENPNGSR----ALRDVRNRFEILD
                                                                                                                                                                                                                                                                                                                                                                                                                         ALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVFLSEQDAVKAAIDIVGKLLTGLGVPFVGPIVSLYTQLIDILWPSKQKSQWEIFMEQVE 120
                                                                                                                                                                                                                                          SLFTQYMPSFRVTNFEVPFLTVYTMAANLHLLLLRDASIFGEEWGLSTSTINNYYNRQMK
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1PR001178; Endotoxin.
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38.8%; Pred. No. 2.7e-70;
tive 141; Mismatches 231; Indels
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ab pests with Bacillus thuringiensis
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                                  InterPro; IPR001178; Endotoxin.
Pfam; PF00555; endotoxin; 1.
                                                                                                                                                      the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein crylib (Insecticidal delta-endotoxin Crylib) (Crystaline entomocidal protoxin) (81 kDa crystal protein).
CRYLIB OR CRYLIG) OR CRYV OR CRYVA65.
                                                                      EMBL; U07642; AAA82114.1; -.
                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95314293; PubMed=7793960;
Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;
"Distribution of cryV-type insecticidal protein genes in Bacillus
thuringiensis and cloning of cryV-type genes from Bacillus
thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          entomocidus.";
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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                                                                                                                           send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                         1. Environ. Microbiol. 61:2402-2407(1995).
FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF CERTAIN COLLOPTERAN AND LEPIDOPTERAN SPECIES.
ACTIVE ON PLUTELLA XYLOSTELLA BUT NOT ON BOMBYX MORI.
DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
                                                                                                                                                                                                                                                                                                       MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNTYIIKGRGYTGGDLVALTDRIGSCEFQMIFPE---SQRFRIRIRYASNETSYISLYGL 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGASVVAGPRFTGGDIIQCTEN-GSAATIYVTPDVSYSQKYRARIHYAS--TSQIT-FTL 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QPNYESYSHRLGHI-TFIYSSSTSTYVPVFSWTHRSADLTNTVKSGEITQIPGGKSSTIG
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                      Sporulation.
   719 AA;
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Best Local Similarity
                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein crylId (Insecticidal delta-endotoxin CryII(d)) (Crystaline entomocidal protoxin) (81 kDa crystal prote
Choi S.-K., Shin B.-S., Kong E.-M., Rho F
"Cloning of a new Bacillus thuringiensis
                                                                                                                        Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                     MEDLINE=20374042; PubMed=10919402;
                                                          STRAIN-BR30
                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             Clid_BACTU
Q9XDL1;
                                                                                                           NCBI_TaxID=1428;
                                                                                                                                                                                                                                                          16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 KTELTRDVLTDPIVGVNNLRGYGTT-----FSNIE-NYIRKPHLFDYLHRIQFH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 TRDYSDHCIKWYNTGLNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 TQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 MFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSASEISTFYNRQVER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 LMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAES 175
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               Rho H.M.,
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crylI-type
                    Park S.-H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - I - DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
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                                                                                                                                                                                                                                                                                                                                                                     DIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVTKVEES-QYNDQTD 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---FSNIE-NYIRKPHLFDYLHRIQFH---TREQPGYYGNDSFNYWSGNYVSTRPSIGSN 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QFRRDMTLMVLDLVALFPSYDTRMYPIPTSAQLTREVYTDAIGTVHPNASFASTTWYNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLRDASIFGKEWGLSESEISTFYNRQSSQTQEYSDYCSEWYNTGLNRLRGTNAESWVRYN 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LESWIEN----RNNTRVRSVVKNQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNSMPSFAISGYEVLFLTTTYAQAANTHLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VASLYSFILGELWPKGKSQWEIFMEHVEELINQKISTYARNKALADLKGLGDALAVYHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLEHNTNMELQNSNHEDCLKMSEYESVEPFVSVST---IQTGIGIAGKILGNLGVPFAGQ
                                                                                                                                                                                                                                                           EASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFLMQGSRGTIPVLT 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYRREMTLTVLDLIALFPLYDVRLYPKEVKTELTRDVLTDPIVGVNNLRGYGTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFN 266
FELSG--NNLQIGVTGLSAGDKVYIDKIEFIPV
                                               INPPFAQRYRLRIRYASTTNLEFHTSINGKAINQGNFSATMNRGEDLDYKAFRTVGFTTP
                                                                                                                                                                                                                                 ASDNFYYPGYAGIGTQLQDSENELPPETTGQPNYESYSHRLSHI--GLISASHVKALVYS 490
                                                                                                                                                                                                                                                                                                                                                                                                                APSFSTIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQY----MNMWGGHKLEFR-TIGGT 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P02965;
                                                                                           PDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLTYNSFNLASFSTP 612
                                                                                                                                        WTHRSADRINTINSDSITQIPLVKAFNLPSGASVVRGPGFTGGDILQRINTGTFGDIRVN
                                                                                                                                                                                 WTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQCTENGSAATIYVT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF047579; AAD44366.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 114; Mismatches 232; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81403 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.5%; Score 1176.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   score 1176.5; DB 1; Length Pred. No. 6.7e-70;
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Best Local Similarity
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16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry7Ab (Insecticidal delta-endotoxin CryVIIA(b)) (Crystaline entomocidal protoxin) (130 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C7AB_BACUK
Q45708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPITHELIAL CELLS OF COLEOPTERA.
-!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis (subsp. kumamotoensis).
Bacteria; Firmicutes; Bacillales; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U04368; AAA21121.1; -. HSSP; P07130; 1DLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coleopteran-active toxins."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Payne J.M., Fu J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-HD867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00555; endotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Coleopteran-active Bacillus thuringiensis isolates and genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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                                                                                                                                                                                                                                                                                      61 TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWP-SEDPWKAFMEQVEALMDQ 119
                                                                                                                                                                                                                                                                                                                                                                 1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ent number US5286486, 15-FEB-1994.
FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF THE SPORE COAT
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                                                                                                                                                                                 KIEQYARNKALAELEGIGNNLTIYQQALEDWINNP---DDPATITRVIDRFRILDALFES 170
                                                                                                                                                                                                                    KIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRN 179
                                                                                                                                                                                                                                                                                                                             MNLNNLGGYE-----DSNRTLNNSLNYPTQKALSPSLKNMNYQDFLSITEREQPEALASG
TRDVLTDPI-VGVNNLRGYGTTFSNIEN-YIRKPHLFDYLHRIQFHT--
                                    SNHCVKWYNSGLSRLNGSTYEQWINYNRFRREMILMVLDIAAVFPIYDPRMYSMÈTSTQL
                                                                                                          YMPSFRVAGYEIPLLTVYAQAANLHLALLRDSTLYGDKWEFTQNNIEENYNRQKKHISEY
                                                                        TDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTEL
                                                                                                                                             SMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEY
                                                                                                                                                                                                                                                      NT--AINTVVSVTGATLSALGVPGASFITNFYLKITGLLWPHDKNIWDEFMTEVETLIEQ 113
                                                                                                                                                                                                                                                                                                                                                                                                     258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sporulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001178; Endotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 114; Mismatches 235; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                     34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129658 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1174.5;
Pred. No. 1.76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E12DC80C0A56D1DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   .5; DB 1;
.7e-69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1138;
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RESULT 10
C77AB_BACUA
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DT 16-OCT
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                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Coleopteran active Bacillus thuringiensis isolates and genes encodicoleopteran active toxins.";
Patent number US5286486, 15-FEB-1994.
-!- FUNCTION: PROMOTES COLEOPTERA.
-!- EPITHELIAL CELLS OF COLEOPTERA.
-!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
                                                                                                                                                                                                   The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTAB_BACUA STANDARD; PRT; 1138 AA. 045707; 045707; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Pesticidial crystal protein cry7Ab (Insecticidal delta-endotoxin CryVIIA(b)) (Crystaline entomocidal protoxin) (130 kDa crystal
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Bacillus thuringlensis (subsp. dakota)

Bacteria; Firmicutes; Bacillales; Baci
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Q45739;
                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein cryIBb (Insecticidal CryIB(b)) (CryStaline entomocidal protoxin) (140
CRYIBB OR CRYIB(B) OR CRYETS.
Donovan W.P., Tan Y., Jany C.S., Gonzalez "Bacillus thuringiensis cryet4 and cryet5 toxic to lepidopteran insects.";
Patent number US5322687, 21-JUN-1994.
                                                                                                       SEQUENCE FROM N.A.
STRAIN-EG5847 / NRRL B-21110;
                                                                                                                                                                                                            Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                          NCBI_TaxID=1428;
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                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 39, Created)
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Pfam; PF00555; endotoxin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 QPGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANT 406
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DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORTLATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESH 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELTROVLTOPIVGVNNLRGYGTT------FSNIENYI-RKPHLFDYLHRIQFHTRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITTAIPLERIRNEEVPLLMVYAQAANLHLLLLRDASLEGSEWGMASSDVNQYYQEQIRYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSAST----VQTGINIAGRILGVLGVPFAGQLASFYSFLVGELWPSGRDPWEIFLEHVEQL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEYSNHCVQWYNTGLNNLRGTNAESWLRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTS 284
                                                   NQYYFDKTINKGDTLTYNSFNLASFSTPFEL--SGNNLQIGVTGLSAGDKVYIDKIEFIP 642
                                                                                                                                                                SVVAGPRETGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPF
                                                                                                                                                                                                                               NYESYSHRLSHI--GLIIGNTLRAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLHSGV
                                                                                                                                                                                                                                                                                                                                                  GTNILFTTPVNGVPWARFNFINPQNIYERGATTYSQPYQGVGIQLFDSETELPPETTERP
                                                                                                                                                                                                                                                                                                                                                                                                      NLAVWPSAVYSGVTKVEFSQYNDQT-DEASTQTYDSK-RNVGAVSWDSIDQLPPETTDEP 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSRWSSTQHMNYWVGHRLNFRPIGGTLNTSTQGLTNNTSINPV-TLQFTSRDVYRTESNA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQLTREIYTDPIGRTNAPSGFASTNWFNNNAPSFSAIEAAIFRPPHLLDFPEQLTIYSA-
NIGNESRIMNRGDNLEYRSFRIAGESTPENFLNAQSTFILGAQSES-NQEVYIDRVEEVP 639
                                                                                                               TVVGGPGFTGGDILRETNTGTFGDIRLNINVPLSQRYRVRIRYASTTDLQFFTRINGTTV 580
                                                                                                                                                                                                                                                                                      LEKGYSHQLNYVMCFLMQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGA 524
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Q45774;
30-MAY-2000
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"Cloning of novel Bacillus thuringlensis delta-endotoxin.";
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
-i- EPITHELIAL CELLS OF INSECTS.
-i- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
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30-MAY-2000 (Rel. 39, Last annotation update)
pesticidial crystal protein cryllac (Insecticidal protein cryllac (Insecticidal protein))
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Bacteria; Firmicutes; Bacillales; Bacillaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 VSAST---VQTGINIAGRILGVLGVPFAGQLASFYSFLVGELWPSGRDPWEIFLEHVEQL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 34.0%; Score 1156.5; DB 1; Length 1233; Local Similarity 37.9%; Pred. No. 3e-68;
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SSRWSSTQHMNYWVGHRLNFRPIGGTLNTSTQGLTNNTSINPV-TLQFTSRDVYRTESNA
                                                                                                                                                                                   TELTRDVLTDPIVGVNNLRGYGTT-----FSNIENYI-RKPHLFDYLHRIQFHTRF 346
                                                                                                                                                                                                                                                                                                            QEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVK 296
                                                                                                                                                                                                                                                                                                                                                                       ITTAIPLFRIRNEEVPLLMVYAQAANLHLLLLRDASLFGSEWGMASSDVNQYYQEQIRYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRQQVTENTRNTAIARLEGLGRGYRSYQQALETWLDNRNDAR---SRSIILERYVALELD 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESH 176
                                                          QPGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANT 406
                                                                                                                         AQLTREIYTDPIGRTNAPSGFASTNWFNNNAPSFSAIEAAIFRPPHLLDFPEQLTIYSA-
                                                                                                                                                                                                                                                  EEYSNHCVQWYNTGLNNLRGTNAESWLRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTS
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                                                                                                                                                                                                          MEDLINE=96178985; PubMed=8606196;
Kostlohka K., Warren G.W., mullins M., Mullins A.D., Palekar N.V.,
Craig J.A., Koziel M.G., Estruch J.J.;
"Cloning of a cryV-type insecticidal protein gene from Bacillus
thuringiensis: the cryV-encoded protein is expressed early in
stationary phase.";
    Selvapandiyan A.,
                                                  STRAIN-61
                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kin Distribution of cryv-type insecticidal protein genes in Buthuringiensis and cloning of cryv-type genes from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tailor R., Tippett J., Gibb G., Pells S., Pike D., Jordan L., Ely S.; "Identification and characterization of a novel Bacillus thuringlensis delta-endotoxin entomocidal to coleopteran and lepidopteran larvae."; Mol. Microbiol. 6:1211-1217(1992).
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"Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for the presence of cryV-like insecticidal protein genes characterization of a cryV gene cloned from B. thuringiensis subspecific that the presence of cryV gene cloned from B. thuringiensis subspecific that the presence of cryV gene cloned from B. thuringiensis subspecific that the protein subspecific that
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MEDLINE-93298009; PubMed-8517758;
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: PROMOTES COLLOIDCSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF CERTAIN COLEOPTERAN AND LEPIDOPTERAN SPECIES.
-CITYE ON PLUTELLA XYLOSTELLA AND BOMBYX MORI.
-I- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
                                                                                                                                                                                                                                                                                                                                                                                          228 AGDYSDHCVKWYSTGLNNLRGINAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 MFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 IINQKISTYARNKALTDLKGLGDALAVYHDSLESWVGN---RNNTRARSVVKSQYIALEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 LMDQKIADYAKNKALAELQGLQNNYEDYYSALSSWQKNPYSSRNPHSQGRIRELFSQAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 FVSAST---IQTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLKNQDKHQSFSSNAKVDKISTDSLK-----NETDIELQNINHEDCLKMSEYENVEP 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MNPNNRSEHDTIKTTEN-NEVPTNHVQYPLAETPNPT---LEDLNYKEFLRMTADNNTEA 56
                                                         ESLAGLNLFLTQPVNGVPRVDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEAT
                                                                                                                                                                                                                                                                                TAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSL
                                                                                                                                                                                                                                                                                                                                    KTELTRDVLTDPIVGVNNLRGYGTT-----FSNIE-NYIRKPHLFDYLHRIQFH--
                                                                                                                                                                                                                                                                                                                                                                                                                                              TQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEV
                                                                                                               VANTNIAVWPSAVYSGYTKVEFS-QYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETT
                                                                                                                                                                         LSRWSNTQY----MNMWGGHKLEFR-TIGGTLNISTQGSTNTSINPV-TLPFTSRDVYRT
                                                                                                                                                                                                                          -TRFQPGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDSSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWP-SEDPWKAFMEQVEA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF THE SPORE COAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M98544; AAA22354.1; -. X62821; CAA44633.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             711
719 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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443
712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81216 MW;
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Pred. No. 1.5e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K -> R (IN STRAIN 61).
D -> Y (IN STRAIN JHCC4835 AND HD-1).
A -> V (IN STRAIN AB88).
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RESULT 14
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                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                          EMBL; M64478; AAA22351.1; -.
EMBL; A07236; CAA00646.1; -.
HSSP; P07130; 1DLC.
InterPro; IPR001178; Endotoxin.
Pfam; PF00555; endotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lambert B., Hofte H., Annys K., Jansens S., Soetaert P., Peferoen M.;
"Novel Bacillus thuringlensis insecticidal crystal protein with a
silent activity against coleopteran larvae.";
Appl. Environ. Microbiol. 58:2536-2542(1992).
-1- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF COLLOPTERA. THIS PROTEIN IS NOT TOXIC IN ITS
NATURAL FORM. IT IS HIGHLY TOXIC TO COLLORADO POTATO BEETILE LARVAE
AFTER AN IN UTIRO SOLUBILIZATION AND TRYPSIN ACTIVATION STEP.
-1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=92384571; PubMed=1514800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CryVIIA(a)) (Crystaline entomocidal protoxin) (129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein cry7Aa (Insecticidal delta-endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C7AA_BACTU
Q03749;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   640
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TTKDVIOKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDP-WKAFMEQVEALMDQ 119
                                                                     MNLNNLDGYE-----DSNRTLNNSLNYPTQKALSPSLKNMNYQDFLSITEREQPEALASG 55
                                                                                                                      MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS 60
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                                                                                                                                                                                                      33.8%;
37.7%;
                                                                                                                                                                                                                                                                              129391 MW;
                                                                                                                                                                            114;
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Pred. No. 4.9e
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                                                                                                                                                                                                                                                                         69D8676D4F6A1FAC CRC64;
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                                                                                                                                                                                                      .9e-68;
                                                                                                                                                                                                                        DB 1;
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                                                                                                                                                                                                                     Length 1138;
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       Seurinck J., Van Audenhove K., Van Rie J., Van Vliet A., Peferoen M "A Bacillus thuringiensis insecticidal crystal protein with a high activity against members of the family Noctuidae.";

Appl. Environ. Microbiol. 62:80-86(1996).

-I- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGU EPITHELIAL CELLS OF LEPIDOPTERA LARVAE. HAS A FAIRLY BROAD SPECTRUM OF ACTIVITY AGAINST MEMBERS OF THE FAMILIES PYRALIDAE, PLUTELLIDAE, SPHINGIDAE, AND NOCTUIDAE. IT IS THE FIRST INSECTICIDAL CRYSTAL PROTEIN WITH ACTIVITY AGAINST CUTWORMS. NO ACTIVITY IS OBSERVED AGAINST SOME BEETLES, SUCH AS COLORADO POT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry9Ca (Insecticidal delta-endotoxin CTYIXC(a)) (Crystaline entomocidal protoxin) (130 kDa crystal
                                                                                                                                                                                                                                                                                                                     STRAIN-BTS02618A;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C9CA_BACTO
Q45733;
                                                                                                                                                                                                                                                                                           MEDLINE=96141404; PubMed=8572715;
                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus thuringiensis (subsp.
Bacteria; Firmicutes; Bacillal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRY9CA OR CRYIXC(A).
                                                                                                                                                                                                                                                              Lambert B., Buysse L., Decock C., Jansens S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEYSDHCTKWYNSGLSRLNGSTYEQWINYNRFRREMILMALDLVAVFPFHDPRRYSMETS 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                       AND PARTIAL SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001178; Endotoxin. Pfam; PF00555; endotoxin; 1. Toxin; Sporulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALD-- 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE SPORE COAT.
MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TERMINUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --SSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDP--WKAFMEQVE
                                                      N--LQIGVTGLSAGDKVYIDKIEFIPVN 644
                                                                                                                                                                                                                                                  SNPQLTREVYTDPIVFNPPANVGLCRRWGTNPYNTFSELENAFIRPPHLFDRLNSLTISS
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QEILTVNAEGVSTGGEYYIDRIEIVPVN
                                                                                                            VRFASTGNFSIRVLRGGVSIGDVRLGSTMNRGQELTYESFFTREFTTTGPFNPPFTFTQA
                                                                                                                                                            IHYASTSQITETLSLDGAPENQYYEDKTINKGDTLTYNSFNLASEST-----PEELSGN 618
                                                                                                                                                                                                                     TPNRITQLPLYKASAPYSGTTYLKGPGFTGGGILRRTTNGTFGTLRYTYNSPLTQQYRLR
                                                                                                                                                                                                                                                                                                                                  NDELPPDESTGSS-----THRLSHVTFFSFQTNQAGSIANAGSVPTYVWTRRDVDLNNTI
                                                                                                                                                                                                                                                                                                                                                                                     IDQLPP-ETTDEPLEKGYSHQLNYVMCFLMQ-----GSRGTIPVLTWTHKSVDFFNMI 504
                                                                                                                                                                                                                                                                                                                                                                                                                                           AVDFRSALI------GIY-GVNRASFVPGGLFNGTTSPANGGCRD------LYDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REOPGYYGNDSENYWSGNYVSTRPSIGSNDIITSPEYG------NKSSEPVQNLEEN
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1088
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988
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Plasmid pBTC19.
Bacteria; Firmicutes; B
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EMBL; AF211190; AAG43526.1; -.
HSSP; P02965; 1CTV.
InterPro; IPR001178; Endotoxin.
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STRAIN-BTC007;
Song F., Zhang J., Huang D., Li
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01-DEC-2001
01-MAR-2002
                                                                                                   SEQUENCE FROM N.A.

Song F., Zhang J., Gu A., Huang D., Li G.;

Son P., Zhang J., Gu A., Huang D., Li G.;

"A novel Crylia endotoxin.";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ

EMBL; AF373207; AAK66742.1; -

InterPro; IPR001178; Endotoxin.

Pfam; PF00555; endotoxin; 1.

SEQUENCE 719 AA; 81225 MW; C629DF2C4482724
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NCBI_TaxID=1428;
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                     MNPNNRSEHDTIKTTEN-NEVPTNHVQYPLAETPNPT---LEDLNYKEFLRMTADNNTEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                            IEFIPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {\tt RTESLAGLNLFLTQPVNGVPRVDFHWKFATLPIASDNFYYLGYAGVGTQLQDSENELPPE}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAVANTNLAVWPSAVYSGYTKVEFSQYNDQTDEASTQTYD-SKRNVGAVSWDSIDQLPPE 459
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                                             33.9%; Score 1155; D: 38.0%; Pred. No. 3.8e tive 132; Mismatches
                                                                                                                                                                                                                                                Bacillus/Clostridium
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Query Match
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
Insecticidal protein.
CRYV101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             085796
                                                                                                                                                           Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Submitted (JUL-1998) to the EMBL/GenBank/DDBJ EMBL; AF076953; AAC26910.1; -. HSSP; P02965; ICIY.
                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid large plasmid.
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                  SEQUENCE
                                                                                                        Pfam;
                                                                                                                                                                                                                                                                            STRAIN-S101
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=29339;
                                                                                                                                                                                                                                                                                                                                                                                                 Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus thuringiensis (subsp. kurstaki).
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                                                                                                           PF00555;
                                                                                                                                      )65; 1CIY.
IPR001178; Endotoxin.
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33.98;
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01-MAR-2002 (TremBLrel.
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                             Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.; "Characterization of crylB gene and its flanking region: "Characterization of cryB gene and its flanking region: Bacillus thuringlensis subsp. encomocidus HD-9."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis (subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                  Delta-endotoxin CrylBa2
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                                                                                                                                                        STRAIN-HD-9;
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  NCBI_TaxID=1436;
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AF363025; AAK51084.1;
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                                                                                                     Bacillaceae;
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38.2%; Pred. No. 7.76
tive 117; Mismatches
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Last sequence up
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01-JUN-2001 (TrEMBLrel. 17, Last ann
                                                        Bacillus thuringiensis.
Bacteria; Firmicutes; E
                                                                                     Delta-endotoxin (Fragment).
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MEDLINE-99025985; PubMed-9806979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00555; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *Assignment of delta-endotoxin genes of the four lepidoptera-specific Bacillus thuringiensis strains that produce spherical parasporal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
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                            O87654;
01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
 Bacillus thuringiensis
                 Delta-endotoxin (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKYPLTDDPNAGLQNMNYKEYLQTYGGDYTDPLINPNLSVSGKDVIQVGINIVGRLLSFF
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                                                                                                                                                                                                                                                                                                                                                                                                             AWRGSRV--RYHYLHSSIIQEKSYGLLSDPVGANINVQNNDIYQIISQVSNFASPVGSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                          YWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVA-----NTNL 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NYNLYVEALDEWLNRPNGAR----ASLVSQRFNILDSLFTQFMPSFG-SGPGSQNYATIL
                                                                                                                                                                    GTTINNFRFTRTMNRGQESRYESYRTVEFTTPFNFTQSQDIIRTSTQGLSGNGEVYLD
                                                                                                                                                                                   GAPFNQYYFDKTINKGDTLTYNSFNLASFSTPFEL--SGNNLQIGYTGLSAGDKVYID 636
                                                                                                                                                                                                                             SSGATYVKGPGETGGDVIRRTNTGGEGAIRVSVTGPLTQRYRIRERYASTIDEDEFVTRG 587
                                                                                                                                                                                                                                                        QSGASVVAGPRFTGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLD 580
                                                                                                                                                                                                                                                                                                                     YSHQLNYVMCFLMQ----GSRGTI----PVLTWTHKSVDFFNMIDSKKITQLPLVKAYKL 520
                                                                                                                                                                                                                                                                                                                                                   SVWDTNFY--LSSGQVSGISGYTQQGIPAVCLQQRN----STDELPSLNPEGDIIRN
                                                                                                                                                                                                                                                                                                                                                                              AVWPSAVYSGVTKVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------GVNNLRGYGTTFSNIEN-YIRKPHLEDYLHRIQFHTREQPGYYGNDSFN 357
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645 AA;
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EMBL; AF093107; AAC63366.1; -.
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MEDLINE=21064760; PubMed=11136135;
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                                                                                                                                                      YSHQLNYV--MCFL--MQGS---RGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQ
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                                                                                                                                                                                                                                                                                                                    ANOGLCRRWRNNPYMTFSELENTFIRPPHLFDRLNSLTINSHRFP--ISSNFMDYWAGH-
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                              APFNQYYFDKTINKGDTLTYNSFNLASFSTPFEL--SGNNLQIGVTGLSAGDKVYID 636
                                                              AGTTVVRGPGFTGGDILRRTSAGTLGTIRVNVNSPLTQRYRVRFRYASTTDFNFFVIRGG
                                                                                                                                                                                                                                                      -TLRRSYMNNSAVQEDSYGATTSTRVTINTGVNGTNRIESTAVDFRSGLLGVYGVHRASF
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TTVNNFTFPRTMNSGQESRYESYVTREFSTSFNFLQIQDTLRLTVQSFSSGQQVYVD
                                                                                SGASVVAGPRFTGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDG
                                                                                                                          -SHRLSHVTFLSFLTDQAGSIRNSGAVPLYVWARQDIDLNNTITANRITQLPLVKASEIA
                                                                                                                                                                                          VPGGLFNGTI----
                                                                                                                                                                                                                      -PSAVYSGVTKVEFSQYNDQTDEASTQTYDSKRNVGAVS-WDSIDQLP-PETTDEPLEKG 468
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638 AA;
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71993 MW;
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598 RYESFATREFTTDFNFRQPQELISVFANAFSAGQEVYFDRIEIIPVN 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shevelev A.B., Svarinsky M.A., Karasin A.I., Kogan Y.N., Chestukhina G.G., Stepanov V.M.;
"Primary structure of the cryx**-the novel Delta-endotoxin-related gene from Bacillus thuringlensis ssp. galleriae.";
FEBS Lett. 336.79-82(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=94085596; PubMed=8262221;
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                    600 TYNSFNLASFSTPFELSGNNLQIGV--TGLSAGDKVYIDKIEFIPVN 644
                                                                                                      540 CTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTL 599
                                                                                                                                                                                                                                                                                        373 LRRNYGSTTS-IVNYFSFNDRDVYQINTRSHTGLGFQNAPLFGITRAQFYPGGTYSVTQR 431
                                                                                                                                                                                                                                                                                                                                                                                                 320 -- TESNIEN-YIRKPHLEDYLHRIQEHTREQPGYYGNDSENYWSGNYVSTRPSIGSNDII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 MTLTVLDLIALFPLYDVRLYPKEVKTELTRDVLTDPIVGVNN------LRGYGT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRYIX GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Delta-endotoxin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 KYGARWGLRESQIGNLYFNELQTRTRDYTNHCVNAYNNGLAGLRGTSAESWLKYHQFRRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 -NGVRANLVLQRFEILHALFVSSMPSFG-SGPGSQRFQAQLLVVYAQAANLHLLLLADAE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 RNPHSQGRIRELFSQAESHFRNSMPSFAISG----YEVLFLTTYAQAANTHLFLLKDAQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 WPSEDP--WKAFMEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 WPSNDQAVWEAFIEQMEELIEQRISDQVVRTALDDLTGIQNYYNQYLIALKEWEERP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 SYKDYLKMSEGDYIDSYINPGNVRTGLQTGIDIVAVVVGALGGPVGGILTGFLSTLFGFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 NYKEFLRMTADNNTEA-LDSSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTI 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                             GINIYSGNLPTYVWTHRDVDLTNTITADRITQLPLVKSFEIPAGTTVVRGPGFTGGDILR 537
                                                                                                                                                                             GSR----GTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQ 539
                                                                                                                                                                                                                                                                                                                                                                AMTFSNLENAIISSPHLFDTINNLMIYTGSFSVHLTNQLIEGWIGHSVTSSLLASGPTTV 372
                                                                                                                                                                                                                   NALTCEQ------NYNSIDELPSLDPNEPISRSYSHRLSHITSYLHRVLTID
                                                                                                                                                                                                                                                   NDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL----MQ 482
                                                                                                                                                                                                                                                                                                                            TSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAV-WPSAVYSGVTKVEF-----SQY 427
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATLMAMDLIALEPYYNTRRYPIAVNPQLTREVYTDPL-GVPSEESSLFPELRCLRWQETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IYGEEWGYEKEDIAEFYKRQLKL-TQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRRE 271
                                                                        RTGVGTFGTIRVRTTAPLTQRYRIRFRFASTTNLFIGIRVGDRQVNYFDFGRTMNRGDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00555; endotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X75019; CAA52927.1; -. P07130; 1DLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001178; Endotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.0%; Score 988; DB 2; 35.4%; Pred. No. 1.3e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129399 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7D28594A19C4B065 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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"Cloning and expression of a delta endotoxin gene from a Chilean native Bacillus thuringiensis strain.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9F296;
Q9F296;
546 INQGNESATMSSGSNLQSGSERTVGFTTPFNFSNGS----SVFTLSAHVFNSGNEVYIDRI
                                                           584 FNQYYFDKTINKGDTLTYNSFNLASFSTPFELSGNNLQIGVTGLSA-----GDKVYIDKI 638
                                                                                                                                                   486
                                                                                                                                                                                             524 ASVVAGPRFTGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAP 583
                                                                                                                                                                                                                                                                   426 FSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPLTKSTNLGSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00555; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U94191; AAG16877.1; -. HSSP; P02965; 1CIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                              469 YSHQLNYVMCFLMQGSRGTI-----PVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSG
                                                                                                                                                                                                                                                                                                                                                                                                    371 FNIGINNQQLSVL-DGTEFA----YGTSSNLPSAVYRKSGTVDSLDEIPPQNNNVPPRQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415 VYSGVTKVEFSQYNDQTDEASTQTYDSKRNVGAVSW-----DSIDQLPPETTDEPLEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 NYWSGNYVSTRPSIGSNDIITSPFYGNK-SSEPVQNLEFN-GEKVYRAVANTNLAVWPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus thuringiensis.
Bacteria; Firmicutes; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 QLTREIYTNPV--LENFDGSFRGSAQGIEGSIRSPHLMDILNSITIYTDAHRGEY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 TTAIPLFAVONYOVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 TKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIW----PSEDPWKAFMEQVEALM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 NPN-----INECIPYNCLS-----NPEVEVLGGE---RIETGYTPIDISLSL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSST 61
                                                                                                                              TSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELTRDVLTDPIVGVNNLRG-YGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NQRIEEFARNQAISRLEGISNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSAL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TQFLLSEFVPGAGFVLGLV-----------DIIWGIFGPSQ--WDAFLVQIEQLI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -YWSGHQIMASPYGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST----LYRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 124;
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(TremBLrel. 16, Last seq
(TremBLrel. 19, Last ann
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 231;
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RESULT 11

Q9AM8

ID Q9AM8

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DT 01-JU

DT 01-Bacl1

OC Bactc

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RN [1]

RN SEQUIT

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus thuringiensis serovar kunthalaRX24.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Bacillaceae; Bacillus.
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01-UN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Insecticidal crystal protein BTRX24.
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Pfam; PF00555; endotoxin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGVVGFPFGGALVSFYTNFLNTIW----PSEDPWKAFMEQVEALMDQKIADYAKNKALAE 132
RRTSPGQISTLRVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSN
                                                                                           GTEFA----YGTSSNLPSAYYRKSGTVDSLDEIPPQNNNVPPRQGFSHRLSHVSMFRSGF
                                                                                                                                                                               QTDEASTQTYDSKRNVGAVSW-----DSIDQLPPETTDEPLEKGYSHQLNYVMCFLMQG
                                                                                                                                                                                                                                                                                                                                                                  RVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV--LE
                   QCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDT 598
                                                                      SNSSYSIIRAPMFSWIHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSYVKGPGFTGGDIL
                                                                                                                                                                                                                     SGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST---LYRRPFNIGINNQQLSVL-D
                                                                                                                                                                                                                                                                                           NFDGSFRGSAQGIEGSIRSPHLMDILNSITIYTDAHRGEY----
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"Molecular characterization of a silent gene encoding a 130-kilodalton crystal protein from Bacillus thuringiensis subsp. israelensis.";

submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF375608; AAK55546.1; -.

InterPro; IPR001178; Endotoxin.

Pfam; PF00555; endotoxin.

Ffam; PF00555; endotoxin; 1.

SEQUENCE 1155 AA; 130747 MW; 7F0C98E0100C7698 CRC64;
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01-JUN-2002 (TrEMBLrel. 2
Crystal protein Crylab16.
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Bacteria; Firmicutes; Bacillus/Clostridium group;
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                                                                                                                                                                                                                                                                                                                                                                           142 TTAIPLEAVQNYRVPLLSVYVQAVNLHLSVLRDVLVFGQRWGEDAATINSRYNDLTRLIG
                                                                                                                                                                                                                                                                                                                                                                                                         178 RNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQ 237
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                                                  FSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPLTKSTNLGSG
                                                                                                                                                                                                               NYWSGNYVSTRPSIGSNDIITSPFYGNK-SSEPVQNLEFN-GEKVYRAVANTNLAVWPSA 414
                                                                                                                                                                                                                                                                                                                             EYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKT
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                                                                                                                                               VYSGVTKVEFSQYNDQTDEASTQTYDSKRNVGAVSW-----DSIDQLPPETTDEPLEKG
                                                                                                                                                                                                                                               QLTREIYTNPV--LENFDGSFRGSAQGIEGSIRSPHLMDILNSITIYTDAHRGEY----
                                                                                                                                                                                                                                                                            ELTRDVLTDPIVGVNNLRG-YGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSF
                                                                                                                                                                                                                                                                                                            NYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVS
                                                                                 YSHQLNYVMCFLMQGSRGTI-----PVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSG
                                                                                                                 FNIGINNQQLSVL-DGTEFA----YGTSSNLPSAVYRKSGTVDSLDEIPPQNNNVPPRQG
                                                                                                                                                                               -YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST
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Pred. No. 1.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
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Agric. Biol. Chem. 48:611-619(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ogo M., Yamada S., Kobayashi Y., Shibata J., Nagamatsu Y., "Nucleotide Sequence of the Lepidoptera-toxic Protein Gene thuringiensis subsp. dendrolimus T84Al.";
J. Fac. Appl. Biol. Sci. Hiroshima Univ. 29:95-107(1990).
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HSSP; P02965; 1CIY.
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Bacillaceae; Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   584 FNOYYFDKTINKGDTLTYNSFNLASFSTPFELSGNNLQIGVTGLSA-----GDKVYIDKI
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  NYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTVLDIVALFSNYDSRRYPIRTVS
                                                                                                                                                                                                                                                                                              TKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIW----PSEDPWKAFMEQVEALM 117
                                         EYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKT
                                                                                  TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIG
                                                                                                                          RNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQ
                                                                                                                                                                                                                                                      TQFLLSEFVPGAGFVLGLV------DIIWGIFGPSQ--WDAFLVQIEQLI
                                                                                                                                                                                                                                                                                                                                         NPN-----INECIPYNCLS-----NPEVEVLGGE---RIETGYTPIDISLSL 42
                                                                                                                                                                                                                                                                                                                                                                              NPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSST 61
                                                                                                                                                                   NQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00555; endotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              28.0%; Score 954.5; DB 2; 33.7%; Pred. No. 2.4e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133489 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                 118;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Hayashi K.;
Protein of Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 105;
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RESULT 14
Q9L877
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                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and sequence analysis of the crylCa6 gene from Bacillus thuringiensis, strain A2-F"; submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF215647; AAF37224.1; -... HSSP; P02955; ICIY. InterPro; IPR001178; Endotoxin. Pfam; PF00555; endotoxin; 1.
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01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=A2-F;
Yu J., Pang Y., Li J.;
                             196
                                                                102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus thuringiensis
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hes 234;
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                                                                                                                                                                                                                                              16 ENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRWTADNNTEALDSSTTKDVIQKGISVVGD 75
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                                                                                                                                                                                                          .3 ENNQ--NQCIPYNCLSNPEEVLLDGE-----RISTGNSSIDISLSLVQFLVSNFVPGGGF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 --FNYWSGHQITASPYGFSGPEFAFPLFGNAGNAAPPVLVSLTGLGIFRTLS-----
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TYAQAANTHLFLLKDAQIYGEEMGYEKEDIAEFYKRQLKLTQEYTDHCVKWYNVGLDKLR
                                                                                                                                                                   LLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQKIADYAKNKALAELQG 135
                                                           LGNNFNIYVEAFKEWEEDP---NNPATRTRVIDRFRILDGLLERDIPSFRISGFEVPLLS
                                                                                            LQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNSMPSFAISGYEVLFLT 195
                                                                                                                                         LVGLIDEVWG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QDNSVPPRAGFSHRLSHVT--MLSQAAGAVYTLRAPTFSWQHRSAEFNNIIPSSQITQIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETTDEPLEKGYSHQLNYVMCFLMQGSRGTI-----PVLTWTHKSVDFFNMIDSKKITQLP
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                                                                                                                                                                                                                                                                                                         27.7%; Score 944.5; DB 2 35.2%; Pred. No. 1.1e-54;
                                                                                                                                                                                                                                                                                                                                                                  134685 MW;
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Bacillus thuringlensis.

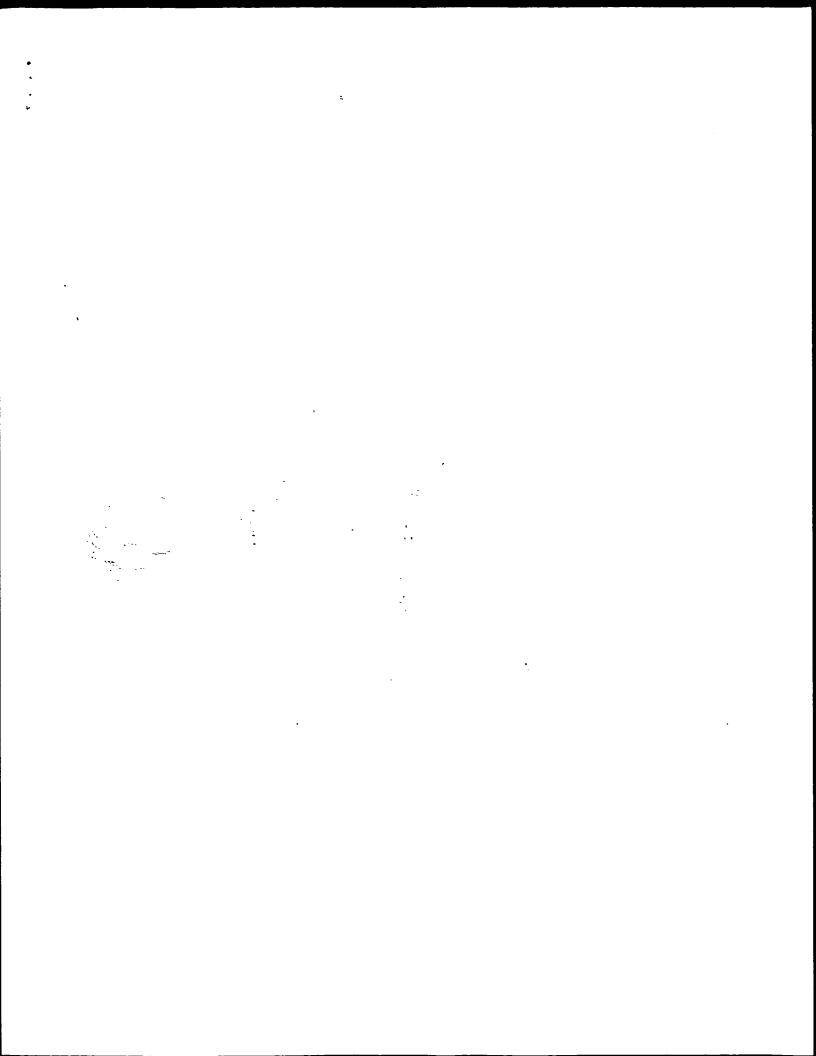
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

Bacillaceae; Bacillus.

NCBI_TaxID-1428;
                                                                                                                                    *Specificity domain localization of Bacillus thuringiensis insecticidal toxins is highly dependent on the bioassay symbol. Microbiol. 14:851-860(1994).
EMBL: U43605; AAA86265.1; -.
HISSP, P02955; 1CIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITINE-95386467; PubMed-7657602;
Masson L., Lu Y.J., Mazza A., Brousseau R., Adang M.J.;
"The CryIA(c) receptor purified from Manduca sexta dispspecificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     045720 PRELIMINARY;
045720;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                 Brousseau R.;
                                                                                                                                                                                                                                                                                                                                                                      STRAIN-NRD-12
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                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                        Masson L.,
                                                                                                                                                                                                                                                                                                                                 MEDLINE-95231292; PubMed-7715447;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 VYAQAANLHLAILRDSVIFGERWGVTTINVNENYNRLIRHIDEYADHCANTYNRGLNNLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 270:20309-20315(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QYYFDKTINKGDTLTYNSFNLASFSTPFELSGNNLQIGVT-----GLSAGDKYYIDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFN-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPSIGSNDIITSPFYGNKSS-EPVQNLEFNGEKVYRAVANTNLAV----WPSAVYS--GV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSVAQLPTENVMESSAIRNPHLEDILNNLTIFT-----DWFSVGRNFYWGGHRVIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGDILRRNTFGDFVSLQVNINSPITQRYRLRFRYAS-SRDARVIVLTGAASTGVGGQVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATEVORSGTPELTTGVVESWTHRSATLTNTIDPERINQIPLVKGERVWGGTSVITGPGFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMQGSRGTIPVLT-----WTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGVEES-----TPTNSFTY----RGRGTV--DSLTELPPEDNSVPPREGYSHRL----CH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGYG--TTFSNIE-NYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFN-----YWSGNYVST
                                                                                    PF00555; endotoxin; 1.
                                                                                                                IPR001178; Endotoxin.
                                                                                                                                                                                                                                                                                                        Mazza A.,
           A.
620
69428 MW;
                                                                                                                                                                                                                                                                                                        Gringorten L.,
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Last annotation update)
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        4571A09E56E56EDE CRC64;
                                                                                                                                                                                                                                                                                                     Baines D., Aneliunas V.
                                                                                                                                                                                                                      bioassay system.";
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Best Local Similarity
Matches 225; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVKAYKLQSGASVVAGPRFTGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQI
                                                                                                                                                                                     ODNSVPPRAGESHRLSHYT--MLSQAAGAVYTLRAPTESWOHRSAEFNNIIPSSQITQIP
                                                                                                                                                                                                                                                                         SAVY-----SG------VTKVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPP
                                                                                                                                                                                                                                                                                                                                                     DSFNYWSGNYVSTRPSIGSNDIITSPFYGNK-SSEPVQNLEFNGEKVYRAVANTNLAVWP
                                                                                                                                                                                                                                                                                                                                                                                    | CITREITTHPV-----LENEDGSFRGMAQRIEQNIRQPHLMDILNSITITTDVHRG----
                                                                                                                                                                                                                                                                                                                                                                                                        RNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIW----PSEDPWKAFMEQVEALM 117
                                                                                        TFTLSLDGAPFNQYYFDKTINKGDTLTYNSFNLASFSTPFELSGNNLQIGVTGLSA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSAL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPN-----INECIPYNCLS-----NPEVEVLGGE---RIETGYTPIDISLSL 42
SGNEVYIDRIEFVP
                           -GDKVYIDKIEFIP
                                                             QFHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTPFNFSNGS----SVFTLSAHVFN
                                                                                                                          LTKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIRYASTTNL
                                                                                                                                                                                                                       ETTDEPLEKGYSHQLNYVMCFLMQGSRGTI-----PVLTWTHKSVDFFNMIDSKKITQLP
                                                                                                                                                                                                                                                        SPLYRRIILGSGPNNQELFVLDGTEFSFASLTTNLPST----IYRQRGTV--DSLDVIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.7%; Score 942.5; DB 2; 33.4%; Pred. No. 5.7e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                    458
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Search completed: January 10, 2003, 11:07:35 Job time: 42 secs



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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                  Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Listing first 100 summaries
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  C 0 8 7 6 5 4 8 8 1
                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein search, using sw model
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Query
Match
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  | SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT: *
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        Length
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                    AAP82487
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AAP95585
AAR39751
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AAR56698
AAY23214
AAW00334
                                                                                                                                                                         AAP70085
  AAY69666
                                                                                                                                                                                                                                                                        SUMMARIES
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                Sequence of toxin
Delta endotoxin en
Amino acid sequenc
M-7 crystal toxin.
Delta endotoxin.
CryIIIA insecticid
CryIIB insecticid
Amino acid sequenc
Bacillus thuringie
                                                                                                                                                                                                             Description
  Wild-type Bacillus
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B.thuringiensis to
B.t.t. coleopteran
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1 CTYIIIA MUTA
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RESULT 1
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DE Cole
XX Micr
XX Micr
XX Baci
XX Micr
XX DP 08-P
XX 16-C
PR 16-C
PR 16-P
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PR 16-P
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DR N-PE
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Best Local
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                                                                                                                                  and expressed. Live mark the killing, the beetles are obtd. The killing, the beetles.
                                                                                                                                                                                                                                                    New poly:peptide toxin having pesticidal activity - forme bacillus thuringiensis toxin gene, and useful for killing Coleoptera beetles
                                                                                                                      Sequence
                                                                                                                                                                                                                       Claim 3; pp15-16; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                       Herrnstadt C,
                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUN-1986;
16-AUG-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus thuringiensis strain san diego
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                                                                                                                                                                                                                                                                                                                                                                                     (MYCO-) MYCOGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microbial pesticide
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                                                                          Local Similarity
                                                                                                                                                         thuringlensis toxin gene toxic to Coleoptera beetles is cloned dexpressed. Live micro-organisms for inhibiting the growth of, lling, the beetles are obtd. The polypeptide toxin may be isola
                                 ш
               MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEELFMTADNNTEALDSS
   MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS
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DB; AAN70092.
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85US-0767227
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AAY23185
                                                                          Score 644;
Pred. No. 0;
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Peptide
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                                          06-MAY-1987;
                                                                       04-MAY-1987;
                                                                                                    17-NOV-1988
                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                               Bacillus
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                                                                                                                                                                                                                                                                                                                    Delta endotoxin encoded by cryC
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        IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS

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                                          87US-0047945
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                                                                                                                                                                        /label=signal_peptide
/note="6 kD"
54..644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Fig 8; 82pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene encoding delta endotoxin of Bacillus thuringiensis ective as insecticide against Coleoptera.
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                                                                                                                                                                                                                                                                                                                                                           DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                                                                                TENGSAATIYYTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
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                                                YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN
                                                                                                   TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
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                                                                                                                                                                                                                                                        The bt13 gene encodes a 66 kDa crystal protein (the Bt13 protein) which is believed to be the active protein in the crystal toxin (the Bt13 toxin) produced by Bacillus thuringlensis (B.t.) tenebrionis and B.t. S1. The patent is for a transformed plant cell which includes, inserted in its genome, the bt13 gene, or a fragment which encodes the 66kD crystal protein. Plant cells contg. DNA encoding this protein are protected against Choleoptera. Also new are plants (and their seeds) contg. these cells; a specific DNA sequence of 1760 b; the crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus thuringiensis tenebrionis; 66 kDa crystal protein; btl3 gene; Btl3 protein; toxin; Coleoptera; pTVE38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUL-1990
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                                                                                                                                                                                                                                                                                                                                                                            Disclosure; ; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                             Plant cell transformed with DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAN91071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaeck M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-DEC-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO8901515-A
                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                protein; and microorganisms transformed with the
                                                                                                                                                                                                                                                                                                                                                                                                     Coleoptera
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                                                                                                                   for Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1989-068871/09.
                                                                 TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
                                                                                                                                                                       644;
                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                     pests
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It
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="As above. It could possibly be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="This residue was not unambiguously determined
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IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS TADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS 180 180

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Pred. No.

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Score 644; Mismatches

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                The gene encoding the toxin can be cloned and used to produce the M-7 crystal which has activity against eg western spotted cucumber beetle, and northern, western and southern corn rootworm.
                                                                             Cloning of Bacillus thuringiensis toxin gene for expression of protein toxic to beetles of
 Sequence
                                                          Disclosure; Page 13-14; 10pp; English.
                                                                                                                                              Hernstadt C,
                                                                                                                                                                                                                                                                            Bacillus thurigiensis strain san-diego (NRRL B-15939).
                                                                                                                                                                                                                                                                                                   M-7 toxin crystal; Coleoptera; beetle.
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                                                                                                                                                                   (MYCO-) MYCOGEN CORP
                                                                                                                                                                                       16-AUG-1985;
15-JUL-1988;
                                                                                                                                                                                                                    30-NOV-1988;
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                                                                                                                  AAN90957
 644 AA;
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                                                                                                                                              Wilcox E;
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88US-0219420
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Best Local Similarity 100.0%;
Matches 644; Conservative 0
(MYCO ) MYCOGEN CORP
                      29-JAN-1992;
                                         31-DEC-1992;
                                                                   05-AUG-1993.
                                                                                        W09314641-A.
                                                                                                           Bacillus thuringiensis PS40D1
                                                                                                                                  Endotoxin; Bacillus; lice; insecticide;
                                                                                                                                                           Delta endotoxin
                                                                                                                                                                                28-JAN-1994 (first entry)
                                                                                                                                                                                                        AAR39751;
                                                                                                                                                                                                                             AAR39751 standard;
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                     92US-0828788
                                           92WO-US11337
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Controlling biting lice on sheep - cor
Bacillus thuringiensis toxins to host
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS
                                                  KVEFSQY\DQTDEASTQTYDSKRNVGAVS\DSIDQLPPETTDEPLEKGYSHQLNYV\CFL
                                                                                                                                                                                                                               GNYVSTRPSIGSNDIITSPFYGNKSSEPVONLEFNGEKVYRAVANTNLAVWPSAVYSGVT
                                                                                                                                                                                                                                                                                      RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTREQPGYYGNDSFNYWS
                                                                                                                                                                                                                                                                                                                                           DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                                                                                                                                                                                                                                                                                                                                                   MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
                                                                                                                                                                                                                                                                                                                                                                                                MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK
YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
                                                                                                                                                              KVEFSQY
                                                                                                                                                                                                                  GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT
                                                                                                                                                                                                                                                                         RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS
                                                                                                                                                                                                                                                                                                                              DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLTALFPLYDVRLYPKEVKTELT
                        YNSFNLASESTPEELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       644;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                      PVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRETGGDIIQC
                                                                                                       NDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 644;
100.0%; Pred. No. 0;
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Best Local S
Matches 644
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11-JUL-1989;
28-AUG-1991;
26-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                            This sequence shows the amino acid sequence of CryIIIA protein. The promoter from the CryIIIA gene sequence was fused to the protein coding region of the CryBII gene (AAQ71027). The recombinant hybrid fusion gene expressed the CryBII crystal protein more efficiently than its native promoter. CryIIB encodes an insecticidal crystal protein isolated from Bacillus thuringlensis var. kurstakl. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CryIIIA insecticidal crystal protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ71026
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                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                      produces crystal proteins during sporulation which are specifically toxic to certain orders and species of insects, esp. Lepidopterans. CryIIB can be used in compositions used as environmentally acceptablinsecticides. (See also AAR56696 and AAR56698)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 7; Fig 4A-4D; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Cry IIB protein - obtd. from the cry II B gene in Bacillus thuringiensis var. Kurstaki, active against lepidopteran insects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Donovan WP;
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241
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                                                                                                                                                                            TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
                                                                                                                                                                                                                   MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS
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                                                                  MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
            DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                                                                                                   IADYAKNKALAELOGLONNVEDYVSALSSWOKNPVSSRNPHSQGRIRELFSQAESHFRNS
                                                                                                                                                            TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK
 DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                      MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
                                                                                                          IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
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44; Conservative
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89US-0379015.
91US-0751452.
93US-0023736.
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Pred. No. 0;
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RESULT 7
ARABSGE 7
ARABSGE 88
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11-JUL-1989;
28-AUG-1991;
26-FEB-1993;
                                       This sequence shows the amino acid sequence of CryIIB protein. The promoter from the CryIIIA gene (AAQ71026) sequence was fused to the protein coding region of the CryBII gene. The recombinant hybrid fusion gene expressed the CryBII crystal protein more efficiently than its native promoter. CryIIB encodes an insecticidal crystal protein isolated from Bacillus thuringiensis var. kurstaki. It
         COXIC
                             produces crystal
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                                                                                                                                                                                                                                                           New Cry IIB protein - obtd. from the cry II B gene in Bac
thuringlensis var. Kurstaki, active against lepidopteran
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CryIIA; CryIIIA; CryIIB; CryC; P-2;
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DB; AAQ71027.
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         certain
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89US-0379015.
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93US-0023736.
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proteins during sporulation which are specifically orders and species of insects, esp. Lepidopterans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                               39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'YC; P-2; CryBI; insecticidal protein
insecticide; Bacillus thuringiensis;
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RESULT 8
AAY23214
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KW Cole
KW Cole
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XX DS Baci
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Best Local
                                                                coleoptera; southern corn rootworm; western corn root worm; Cry3A; Diabrotica undecimpunctata howardi Barber; transgenic plant; Diabrotica virgifera vergifera LeConte; insecticide resistance.
                                                                                                              Cry3Bb; mutant; insecticidal activity; insecticidal specificity;
                                        Bacillus thuringiensis
                                                                                                                                            Amino acid sequence of Cry3A protein.
                                                                                                                                                                            24-AUG-1999
                                                                                                                                                                                                                                  AAY23214 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               describes new Bacillus thuringiensis Cry3Bb mutant proteins, and composition methods for producing them. The B. thuringiensis Cry3Bb CC polypeptide was modified to have improved insecticidal activity or cenhanced insecticidal specificity against a trarget insect. The composition in the primary sequence of the native or unmodified Cry3Bb CC polypeptide, wherein the substitution or deletion occurs at a position cc corresponding to from about amino acids 1-365 of the unmodified cry3Bb CC polypeptide sequence (AAY23207 represents the wild type Cry3Bb CC polypeptide sequence (AAY23207 represents the wild type Cry3Bb CC protein). The polypeptide can be used to kill coleopteran pests, CC especially by application to the environment. It is especially cuseful against southern corn rootworm and western corn root worm, CC (Dlabrotica undecimpunctata howardi Barber, and Dlabrotica virgifera vergifera LeConte respectively). The mutant cry3Bb polynucleotides CC can also be used to produce transgenic plants with increased con secticide resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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18-DEC-1997;
18-DEC-1997;
18-DEC-1997;
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DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
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                                                          RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS
                                                                        RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS
                                                                                                                  DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLTALFPLYDVRLYPKEVKTELT
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Walters FS;
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24-SEP-1983;
04-APR-1986;
09-SEP-1988;
28-JAN-1992;
03-MAY-1993;
                                   The synthetic Btt gene sequence (AAT40340) differs from the native sequence as found in p544Pst-Met5 (AAT40341). Changes in amino acids occur in the synthetic sequence with alanine replacing threonine at residue 2 and leucine replacing the stop at residue 596 followed by the addition of 13 amino acids at the C-terminus. At least 33% of the codons and/or at least 11% of the nucleotides in the coding sequence of the native Bt gene are changed. By avoiding codon usage that are rare in plants, plants that have more Bt crystal protein than plants contg. the native Bt gene, and are thus more toxic to insect pests such as tobacco hornworm, can be
                                                                                                                                                                                                                                                        WPI; 1996-484994/48.
N-PSDB; AAT40341.
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Sequence
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                                                                                                                                                                                                                 Bacillus thuringiensis gene expression requency of codon usages that are rare i
                                                                                                                                                                                                                                                                                              Merlo DJ,
 597
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83US-0535354.
86US-0848733.
88US-0242482.
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                                                                                                                                                                                                                                                                                                                                                    92US-0827844.
93US-0057191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 83US-0535354
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                                                                                                                                                                                                                                                                                                                          SCI INC
                                                                                                                                                                                                                                                                                              Murray EE,
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Best Local Similarity

92.7%; 100.0%;

Score 597; Pred. No.

DB 17; 0;

Length

597;

Query Match

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RESULT 10
AAY69666
IDY 6866
IDY 6866
IDY 6866
AXX AAY6
XX W114
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XX W156
XX US66
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                                                                                                                  09-SEP-1988;
28-JAN-1992;
03-MAY-1993;
                        Murray
                                                                (MYCO ) MYCOGEN PLANT SCI INC
                                                                                                                                                                                          06-JAN-1995;
                                                                                                                                                                                                                                                                                      18-JAN-2000
                                                                                                                                                                                                                                                                                                                                     US6015891-A
                                                                                                                                                                                                                                                                                                                                                                                  Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                    insecticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bt toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wild-type Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY69666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YFDKTINKGDTLTYNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGPRFTGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGPRETGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELFSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFMEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFMEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAVWPSAVYSGVTKVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEK
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                        EE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon usage;
                      Adang
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                                                                                                                  88US-0242482.
92US-0827844.
93US-0057191.
                                                                                                                                                                                       95US-0369835
                                                                                                                                                                                                                                       96US-0705438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thuringiensis (Bt) toxin.
                                                                                                                                                                                                                                                                                                                                                                                  var.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic plant;
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Best Local Similarity Matches 597; Conserv

Conservative

0;

92.7%;

Score 597; Pred. No. Mismatches

0; DB 21; 0

Length 597;

0

Query Match

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The invention relates to a novel synthetic Bacillus thuringiensis (Bt) Coxin gene (AAZ59994) which is expressed at a high level in descendant plant cells and encodes a pesticidal protein toxin. The synthetic gene was designed to be expressed in plants at a higher level than wild type CB the genes (e.g., AAZ59993). This was accomplished by altering the DNA CS sequence of of the native Bt gene such that it contained codons compared by highly expressed plant genes, had an A+T content comparable to that found in plant genes and contained a plant initiation sequence. Additionally, sequences that cause destabilisation, inappropriate CC polyadenylation, degradation and termination of RNA were eliminated, and sequences that constitute RNA hairpin and splice sites were avoided. The resulting synthetic Bt gene has at least 10% of its nucleotides altered as compared with the native Bt gene. The synthetic Bt gene is used to produce transgenic plants having cresistance to pests, particularly insects. The modifications produced in the coding sequence increases the level of expression of Bt toxin in plants. The present sequence represents wild-type Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-136460/12.
N-PSDB; AAZ59993.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic Bacillus thuringiensis pesticidal toxin gene for expression in plant cells has coding sequence adapted to codon usage bias of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example
                                        (var. tenebrionis, Btt) Bt toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Columns 31-36;
597 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
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Q 밁 Š 망 Qy 밁 밁 Q 밁 Ş 밁 ρy Вb Ş Q 밁 В Q 588 481 421 361 408 301 348 241 181 228 121 168 61 48 r GYSHQLNYVMCFLMQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVV YFDKTINKGDTLTYNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN AGPRFTGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPENQY 587 GYSHQLNYVMCFLMQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVV LAVWPSAVYSGVTKVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEK LAVWPSAVYSGVTKVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEK FYKRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFURYRREMTLTVLDLIALFPLYD ELFSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAE AFMEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIR 167 PGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTN FYKRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYD MTADNNTEALDSSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWK 107 AGPRFTGGD11QCTENGSAAT1YVTPDVSYSQKYRAR1HYASTSQ1TFTLSLDGAPFNQY PGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTN ELFSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAE AFMEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIR MTADNNTEALDSSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWK 0 Gaps 527 420 467 407 347 60 480 360 300 240 180 287

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                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                            The sequence is that of an insecticidal protein functionally eqivalent to a native Bt protein. Plant cells expressing the protein have protection against insect damage. Differences between this sequence an that of the wild type comprise the replacement of Thr(2) and STOP(596) with Ala and Leu resp. and the addn. of 13 AAs to the C-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic insecticidal crystal protein gene - comprises DNA sequence encoding insecticidal protein functionally equiv. to bacillus thurigiensis (Bt) insecticidal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adang
                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; ; p; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LUBR ) LUBRIZOL GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP359472-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic Bacillus thuringiensis
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    303
                                                243
                                                                                             183
                                                                                                                                          123
                                                                      290
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                                                                                                                                                                                                                                                                                       Local
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ADNNTEALDSSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAF 109
                                                        LYPKEVKTELTRDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPG
                                                                                                       KRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR
                                                                                                                                                   FSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFY
                                                                                                                                                                                                MEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIREL
                                                                                                                                                                                                                              ADNNTEALDSSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAF
                                            LYPKEVKTELTRDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPG
                                                                                          KRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR
                                                                                                                                                                                  MEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIREL
                                                                                                                                       FSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFY
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                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ03587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rocheleau TA,
                                                                                                                                                                                                                                                                                                                          610 AA;
                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insecticide; crystal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88US-0242482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89EP-0309069
                                                                                                                                                                                                                                                                         92.4%; 5cc
100.0%; Pr
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Merlo
                                                                                                                                                                                                                                                                                       Score 595;
Pred. No.
                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murray
                                                                                                                                                                                                                                                                                                   DΒ
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                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                  610;
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                      409
                                             302
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RESULT 12
ARAWO0333
ADWO0333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JAN-1995;
24-SEP-1983;
04-APR-1986;
09-SEP-1988;
28-JAN-1992;
                                                                       The synthetic Btt gene sequence (AAT40340) differs from the native sequence as found in p544Pst-Met5 (AAT40341). Changes in amino acids occur in the synthetic sequence with alanine replacing threonine at residue 2 and leucine replacing the stop at residue 596 followed by the addition of 13 amino acids at the C-terminus. At least 32% of the codons and/or at least 11% of the nucleotides in the coding sequence of the native Bt gene are changed. By avoiding codon usage that are rare in plants, plants that have more Bt crystal protein than plants contg. the native Bt gene, and archanged.
Sequence
                                                      produced
                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               Increasing Bacillus thuringiensis gene expression in plants reducing frequency of codon usages that are rare in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT40340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MYCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-SEP-1983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus thuringiensis; plant; codon; crystal protein; Btt gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1996-484994/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Merlo DJ,
  610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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83US-0535354.

86US-0848733.

88US-0242482.

92US-0827844.

93US-0057191.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murray EE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pesticidal protein toxin (synthetic).
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Query Match

92.48;

Score 595;

DB 17;

Length 610,

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                                                     06-JAN-1995;
09-SEP-1988;
28-JAN-1992;
                                                                                                                                                                                                                                                            Bt toxin
                                                                                                                                                                                                                                                                                                                  08-MAY-2000
                                                                                                                                                                                                                                                                                                                                              AAY69667
                                           03-MAY-1993;
                                                                                                               29-AUG-1996;
                                                                                                                                           18-JAN-2000
                                                                                                                                                                                                                 Bacillus thuringiensis var. tenebrionis
                                                                                                                                                                                                                                                                                                                                                                          AAY69667
                                                                                                                                                                                                                                              insecticide;
              (MYCO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DKTINKGDTLTYNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKTINKGDTLTYNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYPKEVKTELTRDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYPKEVKTELTRDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTREQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIREL
              MYCOGEN
                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                      thuringiensis (Bt) toxin
                                                                                                                                                                                                                                                           codon usage; expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                              mutant; mutein.
                                                                                                                                                                                                                                                                                                                  (first entry)
                                         95US-0369835.
88US-0242482.
92US-0827844.
93US-0057191.
                                                                                                               96US-0705438
              PLANT SCI INC
                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                           transgenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 595;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murray EE,
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 DKTINKGDTLTYNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN
                            VWPSAVYSGVTKVEFSQVNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGY
                                                                                                                                                                                                                   YYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLA
                                                                                                                                                                                                                                                            LYPKEVKTELTROVLTOPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPG
                                                                                                                                                                                                                                                                          LYPKEVKTELTRDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLEDYLHRIQFHTRFQPG
                                                                                                                                                                                                                                                                                                                   KRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR
                                                                                                                                                                                                                                                                                                                                  KRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR
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                                                                                   SHQLNYVMCFLMQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAG
                                                                                                                 SHQLNYVMCFLMQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAG
                                                                                                                                             VWPSAVYSGVTKVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGY
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nilarity 100.0%;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Extending host range or toxicity of insecticidal proteins protein capable of binding to gut epithelium of insects
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Autographa californica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chimeric; fusion protein; insecticide; AcNPV; Lepidoptera larvae; midgut targetting; bacterial endotoxin; pFX7.
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                                      KRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR
                                                                                  FSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFY
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                                                                       FSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFY
                                                                                                                       MEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIREL
                                                                                                                                              MEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIREL 169
                                                                                                                                                                       ADNNTEALDSSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAF
                        KRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR
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Pred. No.
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in of AcNPV
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carboxyl terminus coding region of B.thuringiensis var. tenebriosis (Btt) toxin. DNA encoding the 9p64 viral membrane protein of ACNPV was operably linked to the Btt toxin coding sequence via the polylinker. The 9p64 gene sequences act as midgut targetting signals for bacterial endotoxins. Of three different Btt/gp64 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chimeric; fusion protein; insecticide; AcNPV;
midgut targetting; bacterial endotoxin; pFAv10
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                                           fusions that were constructed, pFAv10 was the longest. amino acid sequence is given here. See also AAQ14807 and AAQ14808.
                                                                                                                                                                                                                                                                                                                Claim 55; Fig 16; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                 Extending host range or toxicity of insecticidal proteins - protein capable of binding to gut epithelium of insects
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                                         Misc-difference
                                                                                                                                               Misc-difference
                                                                                                                                                                                     Bacillus
                                                                                                                                                                                                                        Bacillus thuringiensis var. tenebrionis; insect resistance; transgenic plant; crop protection; crystal protein; toxin;
                                                                                                                                                                                                                                                                                           04-DEC-1996
                                                                                                                                                                                                                                                                                                                                            AAR99960 standard;
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                                                                                                                                                                                   thuringiensis var.
                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                 /note=
77
                                                                /note-
490
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536
                                                                                          /note=
             /note= "C-terminus 582
                                                                                                                                               Location/Qualifiers 48
                                                                                                                                                                                                                                                               toxin (alternative N- and C-terminal truncations).
                                                                                                                                "N-terminus of construct
"C-terminus
                                                   "C-terminus
                                                                            "N-terminus
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                                                                                                                                                                                    tenebrionis
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric plant gene which expresses a Bacillus thuringiensis toxin protein - useful for prodn of plants which are toxic to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coleopteran insects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-403991/41
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            421
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                                                             MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
                        KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
                                                                                                                                                                                                                                                                                                                                                                              MINNINSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS
                                                                                                                                                                                                                                                                                                                                                                                                       MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS
            KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHELNYVMCFL
                                                                                                                 RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS
                                                                                                                                           RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS
                                                                                                                                                                     DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                                                                                                                                                 DHCVKWYNVGLDKLRGSSYESWVNFNRYRREWTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                                                                                                                                                                                                                                                        IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
                                                                                                                                                                                                                                                                                                                           TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
                                                                                                                                                                                                                                                                          IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
                                                                                                                                                                                                                                                                                                                                          TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
                                                                                                                                                                                                                        MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity
643; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      644 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig 10; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 543;
Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  construct 5448"
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Length 644;

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Gaps

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420

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360 300 240

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ARESULT 17
AAW34811
IID AAW34814
XX AAW34
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KW INCRE
KW CITYII
KW INCRE
KW PEH Key
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                         Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning mutagenesis of domain II of the CryIIIA protein of Bacilius thuriengensis. All that positions changed to alanine in these proteins are located in some of the solvent exposed loops and beta-strands directed towards or located at the molecular apex. The substituted amino acids have a relative solvent accessibility of at least 40%, or are a maximum distance of 3 amino acids away from an amino acid having at least 40% relative solvent accessibility. The novel CryIIIA proteins have an increased toxicity to Coleopteran insects, e.g. Colorado potato beetle, and can be used to combat, or improve plant resistance towards insects. Specifically, the toxicity of the present sequence towards Diabrotica Virgifera virgifera was tested. The ECSO value (concentration at which 50% feeding inhibition is observed) of the present protein was found to be >243 microgram per millilitre; compared to 7.45 microgram per comparing the protein is mutant protein is recognised as a "down mutant" for Diabrotica virgifera virgifera. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5659123-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diabrotica virgifera virgifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
increased toxicity; Coleopteran insect; Colorado potato beetle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel CryIIIA mutant protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects, e.g. corn rootworm and Colorado potato beetle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jansens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PLBZ ) PLANT GENETIC SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-AUG-1994;
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      toxicity of the mutant protein
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relative solvent_accessibility; plant resistance;
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      Diabrotica pest was
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                                                                                                                                                                                                                                DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
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                                         MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
                                                                                                                                                   KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
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                    YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
                                                                                                                                       KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
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YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN
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RESULT 18
AAW34812
cryIIIA gene; corn rootworm toxicity; CryIIIA protein; increased toxicity; Coleopteran insect; Colorado potat relative solvent accessibility; plant resistance;
                                                                                      Novel CryIIIA mutant protein L251A.
                                                                                                                                                     AAW34812 standard;
                                       Diabrotica
                                                                                                             25-FEB-1998
                                      virgifera
                                                                                                            (first entry)
                                                                                                                                                     Protein;
                                                            potato
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beetle;

Bacillus Synthetic

thuriengensis

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DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                                                                                                                       MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKBQLKLTQEYT
                                                                   DHCVKWYNVGADKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                                                                                                      MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
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        IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS

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В S В Ş В Š 밁 Ş

Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning mutagenesis of domain II of the CryIIIA protein of Bacillus thuriengensis. All the positions changed to alanine in these proteins are located in some of the solvent exposed loops and beta-strands directed towards or located at the molecular apex. The substituted amino acids have a relative solvent accessibility of at least 40%, or are a maximum distance of 3 amino acids away from an amino acid having at least 40% relative solvent accessibility. The novel CryIIIA proteins have an

increased toxicity to Coleopteran insects, e.g. Colorado

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RESULT 19
AAW34813
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                                                                                                                                         Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects, e.g. corn rootworm and Colorado potato beetle
                                                                                                                   Example 1; Page -; 22pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus
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                                                                                                                                                                                                                                          PLANT GENETIC SYSTEMS
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                                                                                                                                                                                                                                                                                                                                                                          /label= G352A
                                                                                                                                                                                                                                                                                                                                                            "wild type Gly replaced with Ala"
                                                                                                                                                                                                                   Van Rie J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Colorado potato beetle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and can be used to combat, or improve plant resistance towards insects. Specifically, the toxicity of the present sequence towards Diabrotica virgifera virgifera was tested. The EC50 value (concentration at which 50% feeding inhibition is observed) of the present protein was found to be 4.11 microgram per millilitre, compared to 7.45 microgram per millilitre for the wild type CryIIIA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               using information provided
cryIIIA gene; corn rootworm toxicity; CryIIIA protein; increased toxicity; Coleopteran insect; Colorado potat relative solvent accessibility; plant resistance;
                                                                                                                                                                               AAW34814 standard;
                                                                    Novel CryIIIA mutant protein N353A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                            (first
                                                                                                                                                                               Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not appear in the specification; it was created
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Pred. No. 0;
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                      potato beetle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutagenesis of domain II of the CryIIIA protein Bacillus
thuriengensis. All the positions changed to alanine in these proteins
crithuriengensis. All the positions changed to alanine in these proteins
criticated in some of the solvent exposed loops and beta-strands
crids have a relative solvent accessibility of at least 40%, or are a
crimaximum distance of 3 amino acids away from an amino acid having at least
40% relative solvent accessibility. The novel CryIIIA proteins have an
crincreased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
crimarimum be used to combat, or improve plant resistance towards insects.
Crincreased toxicity of the present sequence towards laest
critically, the toxicity of the present sequence towards laest
critically, the toxicity of the present sequence towards laest
critically inhibition is observed) of the present protein was found to
compared to 11.60 microgram per
critically inhibition is observed) of the present protein was found to
compared to 11.60 microgram per
critically inhibition of the wild type CryIIIA protein.
                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects, e.g. corn rootworm and Colorado potato beetle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                       TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                 DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT 300
                                                                                   MPSFAISGYEVLFLTTYÄQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKROLKLTQEYT
                                                                                                                                                                       IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
                                                                                                                                                                                                     TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK
                                                                   MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
                                                                                                                                     IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
                                                                                                                                                                                                                                                                                                                                            643;
                                                                                                                                                                                                                                                                                                                                                                                                                                            information provided.
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                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                           84.3%;
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                                                                                                                                                                                                                                                                                                                                                            Score 543;
Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                              DB 18;
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                                                                                                                                                                                                                                                                                                                                                                            Length 644;
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Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning mutagenesis of domain II of the CryIIIA protein of Bacillus thurlengensis. All the positions changed to alanine in these proteins are located in some of the solvent exposed loops and beta-strands
                                                                                                                                          Example 1; Page -; 22pp;
                                                                                                                                                                                                                                                       Modified
                                                                                                                                                                                                                                                                                                         WPI; 1997-424316/39.
                                                                                                                                                                                                                                                                                                                                                              Jansens S,
                                                                                                                                                                                                                                                                                                                                                                                                             (PLBZ ) PLANT GENETIC SYSTEMS NV.
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                 601 YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
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                                                                                   TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
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                                                                TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
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        IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS

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Novel CryIIIA mutant protein P412A.

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                                                                                                                                                                                             Matches
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Best Local
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                                                                                                                                                                                                                                                            Sequence
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increased toxicity; Coleopteran insect; Colorado potato beetle;
relative solvent accessibility; plant resistance;
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                IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS 180
                                                                               TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
                                                              TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
TADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
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                                                                                                                                                                                                                                                                                                                                  AAW34817 standard;
Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects,
                                                                                                                                       US5659123-A
                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                     increased toxicity; Coleopteran insect; Colorado relative solvent accessibility; plant resistance
                                                                                                                                                                                                                                                          cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
                                                                                                   26-AUG-1994;
                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                    Bacillus
                                                                                                                                                                                                                               Diabrotica virgifera virgifera.
                                                                                                                                                                                                                                                                           Novel CryIIIA mutant protein S413A.
                                                                                                                                                                                                                                                                                             25-FEB-1998 (first entry)
                            WPI; 1997-424316/39
                                                              (PLBZ ) PLANT GENETIC SYSTEMS NV
                                                                                 26-AUG-1994;
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                                                                                                                                                                                                   thuriengensis
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                                                                                                                                                        /note=
                                                                                                                                                                 'label= S413A
                                                                                                                                                                                                                                                                                                                                 Protein;
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                                                                                                                                                       "wild type Ser replaced
                                              Rie
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                                                                                                                                                                                                                                               Colorado potato beetle;
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.g. corn rootworm and Colorado potato beetle

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC mutagenesis of domain II of the CryIIIA protein of Bacillus thuriengensis. All the positions changed to alanine in these proteins CC thuriengensis. All the positions changed to alanine in these proteins CC are located in some of the solvent exposed loops and beta-strands CC directed towards or located at the molecular apex. The substituted amino CC acids have a relative solvent accessibility of at least 40%, or are a CC maximum distance of 3 amino acids away from an amino acid having at least CC 40% relative solvent accessibility. The novel CryIIIA proteins have an CI increased toxicity to Coleopteran insects, e.g. Colorado potato beetle, CC and can be used to combat, or improve plant resistance towards insects. CC virgifera virgifera was tested. The ECSO value (concentration at which CC 50% feeding inhibition is observed) of the present protein was found to CC be 1.93 microgram per millilitre, compared to 5.55 microgram per CC mote: this sequence for annear in the specification if was created CC this process of the present protein was found to CC be 1.93 microgram per millilitre, compared to 5.55 microgram per CC mote: this sequence for annear in the specification.
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                                  YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN
                                                                      TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
                                                                                            TENGSAATIYVTPDVSXSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            644 AA;
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TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK

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RESULT 24
AAW34818
ID AAW34
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KW CIYII
CC C AITC
CC C AITC
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Ct thuriengensis of domain II of the CryIIIA protein of Bacillus

Ct thuriengensis. All the positions changed to alanine in these proteins

Ct are located in some of the solvent exposed loops and beta-strands

Ct acids have a relative solvent accessibility of at least 40%, or are a

Ct maximum distance of 3 amino acids away from an amino acid having at least

Ct increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,

Ct increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,

Ct and can be used to combat, or improve plant resistance towards insects.

Ct Specifically, the toxicity of the present sequence towards Diabrotica

Ct Virgifera virgifera was tested. The EC50 value (concentration at which

Ct of feeding inhibition is observed) of the present protein was found to

Ct of 156 microgram per millilitre, compared to 5.55 microgram per

Ct mote: this sequence does not appear in the specification; it was created
                         Query Match
Best Local S
   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects, e.g. corn rootworm and Colorado potato beetle
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                                                                                                                        Sequence
                                                                                                                                                                                  using information provided
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                               Similarity
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'note= "wild
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                            84.3%;
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Pred. No. 0;
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Mismatches
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                                                         Length 644;
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                                                                                                                                                                                  26-AUG-1994;
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   Jansens
                                                           (PLBZ ) PLANT GENETIC SYSTEMS NV
                                                                                                                          26-AUG-1994;
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   Peferoen M,
                                                                                                                          94US-0295060
                                                                                                                                                                                  94US-0295060.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                'label- Q411A
                                                                                                                                                                                                                                                                                                                                                                 "wild type Trp replaced
      Van Rie J;
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Sequence

BG 18;

Length 644;

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CC mutagenesis of domain II of the CryIIIA protein of Bacillus chiral there is of domain II of the CryIIIA protein of Bacillus chiral there is of domain II of the CryIIIA protein of Bacillus chiral there is the selection of Bacillus controlled in some of the solvent exposed loops and beta-strands coldishave a relative solvent accessibility of at least 40%, or are a calds have a relative solvent accessibility of at least 40%, or are a commanded to accessibility. The novel CryIIIA proteins have an increased toxicity to Coleopteran insects, e.g. Colorado potato beetle, concan be used to combat, or improve plant resistance towards insects. CC specifically, the toxicity of the present sequence towards insects. CC virgifera virgifera was tested. The EC50 value (concentration at which compared to 3.86 microgram per millilitre, compared to 3.86 microgram per compared to 3.86 microgram per millilitre, compared to 3.86 microgram per compared as a "down mutant" for Diabrotica virgifera virgifera. The conjusted as a "down mutant" for Diabrotica virgifera virgifera. The conjusted as a "down mutant" for Diabrotica virgifera virgifera. The conjusted with the toxicity of the matant protein for this Diabrotica per was created content the sequence does not appear in the specification; it was created content information out appear in the specification; it was created contents in formation out appear in the specification; it was created contents of the present in the specification; it was created contents of the present in the specification; it was created contents of the present in the specification; it was created contents of the present in the specification; it was created contents of the present in the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified Bacillus thuringlensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects, e.g. corn rootworm and Colorado potato beetle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-424316/39
                                                                     information provided.
   644 AA;
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В 밁 γ DЪ Š В Š 밁 ò 밁 γΩ 밁 Q Š Query Match Best Local Matches 421 361 361 301 301 241 241 181 181 121 121 61 61 Local Similarity es 643; Conserv 1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS 1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120 KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL 480 GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVAPSAVYSGVT Conservative 84.3%; 0; Score 543; Pred. No. 0; Mismatches 1; Indels 0 Gaps 300 180 120 60 420 360 300 240 240 0

Вb

541 481 481 421

TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT

600

540

MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC MQGSRGTIPVLTWTHKSVDFENMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC 밁

KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL

Matches 643;

Conservative

0,

Mismatches

Indels

0,

0

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RESULT 26
AAW34020
ID AAW34020
AAW3402
AAW34020

                                                                                                                                                    thurlengensis. All the positions changed to alanine in these proteins are located in some of the solvent exposed loops and beta-strands directed towards or located at the molecular apex. The substituted amino acids have a relative solvent accessibility of at least 40%, or are a maximum distance of 3 amino acids away from an amino acid having at least 40% relative solvent accessibility. The novel CryIIIA proteins have an increased toxicity to Coleopteran insects, e.g. Colorado potato beetle, and can be used to combat, or improve plant resistance towards insects. Specifically, the toxicity of the present sequence towards insects. Specifically, the toxicity of the present sequence towards Diabrotica collisions of the present sequence towards protein acceptable of the present protein was found to be 5.50 microgram per millilitre, compared to 2.42 microgram per millilitre for the wild type CryIIIA protein.

CC mate: this sequence does not appear in the specification; it was created contents the sequence does not appear in the specification; it was created contents the sequence does not appear in the specification.
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   Best Local Similarity
                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning mutagenesis of domain II of the CryIIIA protein of Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects, e.g. corn rootworm and Colorado potato beetle
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                                                                                         Sequence
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Matches 643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning mutagenesis of domain II of the CryIIIA protein of Bacillus thuriengensis. All the positions changed to alanine in these proteins are located in some of the solvent exposed loops and beta-strands directed towards or located at the molecular apex. The substituted amino acids have a relative solvent accessibility of at least 40%, or are a maximum distance of 3 amino acids away from an amino acid having at least 40% relative solvent accessibility. The novel CryIIIA proteins have an increased toxicity to Coleopteran insects, e.g. Colorado potato beetle, and can be seed to coleopteran insects, e.g. Colorado potato beetle,
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                          Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning mutagenesis of domain II of the CryIIIA protein of Bacillus thuriengensis. All the positions changed to alanine in these proteins are located in some of the solvent exposed loops and beta-strands directed towards or located at the molecular apex. The substituted amino acids have a relative solvent accessibility of at least 40%, or are a maximum distance of 3 amino acids away from an amino acid having at least 40% relative solvent accessibility. The novel CryIIIA proteins have an increased toxicity to Coleopteran insects, e.g. Colorado potato beetle, and can be used to combat, or improve plant resistance towards insects. Specifically, the toxicity of the present sequence towards Diabrotica virgifera was tested. The ECSO value (concentration at which 50% feeding inhibition is observed) of the present protein was found to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diabrotica virgifera virgifera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects,
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   1.09 microgram per millilitre,
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   is observed) of the present protein was found millilitre, compared to 1.21 microgram per
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Best Local
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                                                              cryIIIA gene; corn rootworm toxicity; CryIIIA protein; increased toxicity; Coleopteran insect; Colorado potat relative solvent accessibility; plant resistance;
                                                                                                                   Novel CryIIIA mutant protein N312A.
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                                                                                                                                                                                                   AAW34823 standard;
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note: this sequence does not appear in the specification;
             Bacillus thuriengensis
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CC thuriengensis of domain II of the CryIIIA protein of Bacillus
CC thuriengensis. All the positions changed to alanine in these proteins
CC are located in some of the solvent exposed loops and beta-strands
CC directed towards or located at the molecular apex. The substituted amino
CC acids have a relative solvent accessibility of at least 40%, or are a
CC maximum distance of 3 amino acids away from an amino acid having at least
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards Diabrotica
CC virgifera virgifera was tested. The EC50 value (concentration at which
CC 50% feeding inhibition is observed) of the present protein was found to
CC to the for the wild type CryIIIA protein.
CC millilitre for the wild type CryIIIA protein.
CC conte: this sequence does not appear in the specification; it was created
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RDVLTDPIVGVANLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS
                                                                                                 DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
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Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning mutagenesis of domain II of the CryIIIA protein of Bacillus thuriengensis. All the positions changed to alanine in these proteins are located in some of the solvent exposed loops and beta-strands directed towards or located at the molecular apex. The substituted amino acids have a relative solvent accessibility of at least 40%, or are a maximum distance of 3 amino acids away from an amino acid having at least 40% relative solvent accessibility. The novel CryIIIA proteins have an increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
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             YNSFNLASFSTDFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
                                                                       TENGSAATIYYTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
                                                                                                                 MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
                                                                                                                                MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
                                                                                                                                                                           KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
                                                                                                                                                                                                                                      GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT
                                                                                                                                                                                                                                                 GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT
                                                                                                                                                                                                                                                                                              RDVLTDPIVGVNNLRGYGTTFSNIEAYIRKPHLEDYLHRIQFHTRFQPGYYGNDSFNYWS
                                                                                                                                                                                                                                                                                                                          RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLEDYLHRIQFHTREQPGYYGNDSFNYWS
                                                                                                                                                                                                                                                                                                                                                       DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                                                                                                                                                                                                                                                                                                                                     DHCVKWYNVGLDKLRGSSYESWVNFNRYRREWTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN
                                                          TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
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RESULT 31
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AC AAW34
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DT 25-FE
XX NOVel
XX CTYII
KW incre
KW relat
               cryIIIA gene; corn rootworm toxicity; CryIIIA protein; increased toxicity; Coleopteran insect; Colorado pota!
                                                                               25-FEB-1998
                                                                                                                                 AAW34825 standard;
                                                    Novel CryIIIA mutant protein
                                                                               (first
                                                                                                                                   Protein;
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                                                      E387A.
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relative solvent

increased toxicity; Coleopteran insect; Colorado
relative solvent accessibility; plant resistance

potato

beetle;

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Content this sequence does not appear in the specification; it was created was ing information provided.
                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning mutagenesis of domain II of the CryIIIA protein of Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page -; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects,
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MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
                                                                                   MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKROLKLTQEYT
                                                                                                                                                IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
                                                                                                                                                                                              TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK
                                                                                                                                                                                                               TTKDVIOKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
                                                                                                                                                                                                                                                          NIPNIRSEHDTIKTTENNEVPTNHVQYPLAETENPTLEDLNYKEFLRMTADNNTEALDSS 60
                                                                                                                             IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
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                                                                                                                                                                                                                                                                                                                                                                                                644 AA;
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99.8%;
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RESULT 3:
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                                                         Example 1; Page -; 22pp; English.
                                                                                          Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects,
                                                                                                                                                         Jansens S,
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                                                                                                                                                                                  (PLBZ ) PLANT GENETIC SYSTEMS NV
                                                                                                                                                                                                                                                                                                                                                                                                 cryIIIA gene; corn rootworm toxicity; CryIIIA protein; increased toxicity; Coleopteran insect; Colorado potat; relative solvent accessibility; plant resistance; Diabrotica virgifera virgifera.
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                                                                                 rootworm and
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                                                                                                                                                                                                                                                                                                     /note= "wild type Lys replaced with Ala"
                                                                                                                                                                                                                                                                                                                   /label= K384A
                                                                               Colorado potato beetle
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Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning mutagenesis of domain II of the CryIIIA protein of Bacillus thuriengensis. All the positions changed to alanine in these proteins are located in some of the solvent exposed loops and beta-strands

solvent exposed loops and beta-strands

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RESULT 33
AAW34827
ID AAW34
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AC AAW34
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AC AAW34
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Matches 643
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                  25-FEB-1998
                                                                             AAW34827 standard;
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information provided.
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Pred. No. 0;
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thuriengensis of domain II of the CryIIIA protein of Bacillus

ct thuriengensis. All the positions changed to alanine in these proteins

cc thuriengensis. All the positions changed to alanine in these proteins

cc are located in some of the solvent exposed loops and beta-strands

cd are located towards or located at the molecular apex. The substituted amino

cc acids have a relative solvent accessibility of at least 40%, or are a

cc maximum distance of 3 amino acids away from an amino acid having at least

cc 40% relative solvent accessibility. The novel CryIIIA proteins have an

cc increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,

cc and can be used to combat, or improve plant resistance towards insects.

cc Specifically, the toxicity of the present sequence towards Diabrotica

cutingifera virgifera was tested. The ECSO value (concentration at which

cc 10% feeding inhibition is observed) of the present protein was found to

cc be 0.78 microgram per millilitre, compared to 2.88 microgram per

cc note: this sequence does not annear in the specification: it was created
                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                            Matches 643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
increased toxicity; Coleopteran insect; Colorado potato beetle;
relative solvent accessibility; plant resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects, e.g. corn rootworm and Colorado potato beetle
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                                                   IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
                                                                                                                       TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK
                                                                                                      TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK
                                                                                                                                                                        MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS
MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
                                 IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
                                                                                                                                                                                                                                                                                                                                                 information provided.
                                                                                                                                                                                                                                                                                                                                                                    this sequence does not appear in the specification; it was created
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                          YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
VNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN
                                                                                             TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
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RESULT 35 AAW34829 ID AAW3

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                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page -; 22pp; English.
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Bacillus thuriengensis
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                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and can be used to combat, or improve plant resistance towards insects. Specifically, the toxicity of the present sequence towards Diabrotica virgifera was tested. The present sequence (concentration at which 50% feeding inhibition is observed) of the present protein was found to be 0.30 microgram per millilitre, compared to 1.39 microgram per millilitre, compared to 1.39 microgram per millilitre for the wild type CryIIIA protein.
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                                               YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN
                                                                                                  TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
                                                                                                                                   TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
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YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN
                                                                                                                                                                                                               MQGSRGTTPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
                                                                                                                                                                                                                                        MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
                                                                                                                                                                                                                                                                                                                         KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
                                                                                                                                                                                                                                                                                                                                                                            KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
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Ct thuriengensis. All the positions changed to alanine in these proteins
Ct thuriengensis. All the positions changed to alanine in these proteins
Ct are located in some of the solvent exposed loops and beta-strands
Ct directed towards or located at the molecular apax. The substituted amino
Ct acids have a relative solvent accessibility of at least 40%, or are a
Ct maximum distance of 3 amino acids away from an amino acid having at least
Ct 40% relative solvent accessibility. The novel CryIIIA proteins have an
Ct increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
Ct and can be used to combat, or improve plant resistance towards insects.
Ct Specifically, the toxicity of the present sequence towards Diabrotica
Ct virgifera virgifera was tested. The ECSO value (concentration at which
Ct 50% feeding inhibition is observed) of the present protein was found to
Ct be 0.33 microgram per millilitre, compared to 1.39 microgram per
Ct millilitre for the wild type CryIIIA protein.
Ct note: this sequence does not appear in the specification; it was created
                                                                                         Query Match
Best Local S
Matches 643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects,
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                                                                                                                                                                                                                                                                                   information provided.
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icity; Coleopteran insect; Colorado pota
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increased toxicity; Coleopteran insect; Colorado potato beetle;
relative solvent accessibility; plant resistance;
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  PLANT
                                                                                                                                                                                                                                                                                                                                                        thuriengensis
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  GENETIC
                                               94US-0295060
                                                                                            9405-0295060
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/note= "wild type
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Matches Query Match Best Local

643;

Conservative

0

Mismatches

Similarity

84.3%;

Score 543; Pred. No. 0;

DB 18;

Length 644;

0

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Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning mutagenesis of domain II of the CryIIIA protein of Bacillus thuriengensis. All the positions changed to alanine in these proteins are located in some of the solvent exposed loops and beta-strands directed towards or located at the molecular apex. The substituted amino acids have a relative solvent accessibility of at least 40%, or are a maximum distance of 3 amino acids away from an amino acid having at least 40% relative solvent accessibility. The novel CryIIIA proteins have an increased toxicity to Colepteran insects, e.g. Colorado potato beetle, and can be acided to combat of the proteins have an increased toxicity to Colepteran insects, e.g. Colorado potato beetle, and can be acided to combat of the proteins have an increased toxicity to Colepteran insects, e.g. Colorado potato beetle, and can be acided to combat of the proteins have an increased toxicity to Colepteran insects, e.g. Colorado potato beetle, and can be acided to combat of the proteins have an increased toxicity to Colepteran insects.
                                                                              and can be used to combat, or improve plant resistance towards insects. Specifically, the toxicity of the present sequence towards Diabrotica virgifera virgifera was tested. The ECSO value (concentration at which 50% feeding inhibition is observed) of the present protein was found to be 4.29 microgram per millilitre, compared to 3.08 microgram per millilitre for the wild type CryIIIA protein.

note: this sequence does not appear in the specification; it was created
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jansens S,
                                                     using information provided.
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644 AA;
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Š 밁 Q 밁 Ş 망 Š 밁 δÃ В δÃ 밁 δÃ Вb Ş ρ 밁 В Q 181 421 361 361 301 241 181 421 301 121 61 61 TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120 1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNAAVWPSAVYSGVT DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELESQAESHFRNS MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLTALFPLYDVRLYPKEVKTELT MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK ب. 0 Gaps 120 480 480 420 420 360 300 240 180 60 60 360 300 180

Similarity

84.38; 99.88;

Score 543; Pred. No.

0 DΒ

Length 644;

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RESULT 3S
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IDW34833
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                                                                              Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning CC mutagenesis of domain II of the CryIIIA protein of Bacillus thuriengensis. All the positions changed to alanine in these proteins CC are located in some of the solvent exposed loops and beta-strands CC directed towards or located at the molecular apex. The substituted amino CC acids have a relative solvent accessibility of at least 40%, or are a CC maximum distance of 3 amino acids away from an amino acid having at least 10% relative solvent accessibility. The novel CryIIIA proteins have an increased toxicity to Coleopteran insects, e.g. Colorado potato beetle, CC and can be used to combat, or improve plant resistance towards insects. Specifically, the toxicity of the present sequence towards insects. CC virgifera virgifera was tested. The EC50 value (concentration at which CC virgifera virgifera was tested. The EC50 value (concentration at which CC is feeding inhibition is observed) of the present protein was found to be 12.47 microgram per millilitre, compared to 3.08 microgram per CC included as a "down mutant" for Diabrotica virgifera virgifera. The CC recognised as a "down mutant" for Diabrotica virgifera virgifera. The CC interesting the mutant protein for this Diabrotica pest was created CC information provided.

CC using information provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page -; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects, e.g. corn rootworm and Colorado potato beetle
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increased toxicity; Coleopteran insect; Colorado
relative solvent accessibility; plant resistance;
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                                                                    information
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t; Colorado potat
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Best Local
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Sequence

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                                                                                                                                                                                                  Synthetic
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                                                                                                                                                                                                                                                                   increased toxicity; Coleopteran insect; Colorado relative solvent accessibility; plant resistance;
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icity; Coleopteran insect; Colorado pota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thurlengensis. All the positions changed to alanine in these proteins are located in some of the solvent exposed loops and beta-strands directed towards or located at the molecular apex. The substituted amino acids have a relative solvent accessibility of at least 40%, or are a maximum distance of 3 amino acids away from an amino acid having at least 40% relative solvent accessibility. The novel CryIIIA proteins have an increased toxicity to Coleopteran insects, e.g. Colorado potato beetle, and can be used to combat, or improve plant resistance towards insects. Specifically, the toxicity of the present sequence towards Diabrotica virgifera was tested. The EC50 value (concentration at which 50% feeding inhibition is observed) of the present protein was found to be 0.39 microgram per millilitre, compared to 0.71 microgram per mote: this sequence does not appear in the specification; it was created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified Bacillus thuringiensis CryIII proteins - with increased
toxicity against insect pests, particularly Coleopteran insects,
e.g. corn rootworm and Colorado potato beetle
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CC mutagenesis of domain II of the CryIIIA protein of Bacillus
CC thuriengensis. All the positions changed to alanine in these proteins
CC are located in some of the solvent exposed loops and beta-strands
CC are located in some of the solvent exposed loops and beta-strands
CC acids have a relative solvent accessibility of at least 40%, or are a
CC maximum distance of 3 maino acids away from an amino acid having at least
CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards insects.
CC virgifera virgifera was tested. The ECSO value (concentration at which
CC 10% feeding inhibition is observed) of the present protein was found to
CC be 0.51 microgram per millilitre, compared to 0.71 microgram per
CC millilitre for the wild type CryIIIA protein.
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increased toxicity; Coleopteran insect; Colorado potato beetle;
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                                                                  cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
increased toxicity; Coleopteran insect; Colorado potato
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using
                      Bacillus
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                                                         increased toxicity; Coleopteran insect; Colorado relative solvent accessibility; plant resistance;
                                                                                                 Novel CryIIIA mutant protein I375A.
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        IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS

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/note= "wild"
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CC Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning CC mutagenesis of domain II of the CryIIIA protein of Bacillus CC thuriengensis. All the positions changed to alanine in these proteins CC are located in some of the solvent exposed loops and beta-strands CC directed towards or located at the molecular apex. The substituted amino CC acids have a relative solvent accessibility of at least 40%, or are a CC maximum distance of 3 amino acids away from an amino acid having at least CC 40% relative solvent accessibility. The novel CryIIIA proteins have an CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle, CC and can be used to combat, or improve plant resistance towards insects. CC Specifically, the toxicity of the present sequence towards Diabrotica CC virgifera virgifera was tested. The EC50 value (concentration at which CC 10% feeding inhibition is observed) of the present protein was found to be 1.65 microgram per millilitre, compared to 0.95 microgram per CC mote: this sequence does not appear in the specification; it was created of information and appear in the specification; it was created content information and appear in the specification; it was created content information and appear in the specification; it was created contents information and appear in the specification; it was created contents information and appear in the specification; it was created contents to the contents and appear in the specification; it was created contents to the contents and appear in the specification; it was created contents to the contents and appear in the specification; it was created contents to the contents and appear in the specification.
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                                                                                       RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS
GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS 60
                                                                                                                                                                                                                                                                                                           DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
                                                                                                                                                                                                                                                                                                                                                                                                             DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
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Pred. No. 0;
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Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning mutagenesis of domain II of the CryIIIA protein of Bacillus thurlengensis. All the positions changed to alanine in these proteins are located in some of the solvent exposed loops and beta-strands directed towards or located at the molecular apex. The substituted amino acids have a relative solvent accessibility of at least 40%, or are a maximum distance of 3 amino acids away from an amino acid having at least 40% relative solvent accessibility. The novel CryIIIA proteins have an increased toxicity to Coleopteran insects, e.g. Colorado potato beetle, and can be used to combat, or improve plant resistance towards insects.
                                                                                                                                                                                                                                                                                                                                                    Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects, e.g. corn rootworm and Colorado potato beetle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
increased toxicity; Coleopteran insect; Colorado potato beetle;
relative solvent accessibility; plant resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             increased tox:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel CryIIIA mutant protein Y416A.
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RESULT 44
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AC NOVE
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XX
CTYI

AAW34838

standard;

Protein;

644

25-FEB-1998

(first entry)

cryIIIA gene;

corn

rootworm toxicity; CryIIIA protein;

Novel CryIIIA mutant protein

Y327A.

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Best Local
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                           YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN
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YNSFNLASESTPEELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN
                                                                                                            TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
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                                                                                                                                                                                                                   MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
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99.8%;
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                                                                                                                                                                                                                                                                                                                                                                Novel CryIIA proteins AAW34811-41 were produced by alanine scanning CC mutagenesis of domain II of the CryIIIA protein of Bacillus thuriengensis. All the positions changed to alanine in these proteins are located in some of the solvent exposed loops and beta-strands directed towards or located at the molecular apex. The substituted amino acids have a relative solvent accessibility of at least 40%, or are a maximum distance of 3 amino acids away from an amino acid having at least 40% relative solvent accessibility. The novel CryIIIA proteins have an increased toxicity to Coleopteran insects, e.g. Colorado potato beetle, and can be used to combat, or improve plant resistance towards insects. Specifically, the toxicity of the present sequence towards Diabrotica virgifera was tested. The ECSO value (concentration at which 50% feeding inhibition is observed) of the present protein was found to be 2.40 microgram per millilitre, compared to 3.82 microgram per millilitre for the wild type CryIIIA protein.
                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects, e.g. corn rootworm and Colorado potato beetle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jansens S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-AUG-1994;
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                                                                                                                                                              TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
                                                                                                                                                                                                                                                 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS 60
DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT 300
                                                                                               IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
                                MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
                                                 MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT 240
                                                                                                                               IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS 180
                                                                                                                                                                                                                                MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS
                                                                                                                                                                                                                                                                                                 643;
                                                                                                                                                                                                                                                                                                                                                                                                information provided.
                                                                                                                                                                                                                                                                                                                                                                                                            this sequence does not appear in the specification; it was created
                                                                                                                                                                                                                                                                                                                                                                  644 AA;
                                                                                                                                                                                                                                                                                                 Conservative
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     Novel CryIIIA proteins AAW34811-41 were mutagenesis of domain II of the CryIIIA
                                                                               Claim 9; Page -; 22pp; English.
                                                                                                                                    Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects, e.g. corn rootworm and Colorado potato beetle
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                                                                                                                                                                                                                                                                                                                                                   (PLBZ ) PLANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
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                                                                                                                                                                                                                                                                                                                                                               GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT 420
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YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
                                                                                                                           TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT 600
                                                                                                                                                                                           MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
                                                                                                                                                                                                                                                       KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
                                                                                                                                                                                                                                                                                               KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL 480
                                                                                                                                                                                                                                                                                                                                        GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT
                                                                                                                                                                                                                                                                                                                                                                                                                            RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRAQPGYYGNDSFNYWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTREQFGYYGNDSFNYWS
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                                                                                   TENGSAATIYVTPDVSYSQKYRARIHYASTSQITETLSLDGAPFNQYYFDKTINKGDTLT
                                                                                                                                                                   MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRETGGDIIQC
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99.8%;
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AAW34840 ID AAW

AAW34840 standard; Protein; 644

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AAW34840

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diabrotica virgifera virgifera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Page -; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e.g. corn rootworm and Colorado potato beetle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects,
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                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                                            using information provided.
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                                  121
                                                                 1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS
                                                                                                                                                                    1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS 60
                                IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS 180
IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS 180
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99.8%;
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RESULT 47
ANA34841
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Modified Bacillus thuringiensis CryIII proteins - with increased toxicity against insect pests, particularly Coleopteran insects, e.g. corn rootworm and Colorado potato beetle
                                                                                                                                                                                                                                                                                     Jansens S,
                                                                                                                                                                                                                                                                                                                                                             (PLBZ ) PLANT GENETIC SYSTEMS NV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   increased toxicity; Coleopteran insect; Colorado relative solvent accessibility; plant resistance; Diabrotica virgifera virgifera.
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US-08-995-1137-4
US-08-993-722A-113
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RESULT 1 US-07-828-788A- US-07-828-788A- Sequence 4, A) Patent No. 52 GENERAL INFO: APPLICANT: TITLE OF II NUMBER OF CORRESPOND ADDRESSE STATE: COUNTRY: SIP: SIP: CUNTRY: COUNTRY: COUNTRY: SOFTWARE CURRENT AP APPLICAT FILLING D CLASSIFI ATTORNEY/AA REFERENC TELEFAA: INFORMATION SEQUENCE C STATE: CHASSIFI ATTORNEY/AA REFERENC TELEFAA: INFORMATION TELEFAA: INFORMATION SEQUENCE CORRENT APPOLOGY MOLECULE I TYPE: ASTRANUE TOPOLOGY MOLECULE I ANTI-SENGE ORIGINAL STRANUE INFORMATION TELEFAA: INFORMATION TORGINAL STRANUE INFORMATION TORGINAL TORGI		44444333333228 444443398765433210998
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8788A ACILLUS THURINGIENSI AGAINST PHTHIRAPTERA ANCHIK REET, SUITE A-1 REET, SUITE A-1 /828,788A /828,788A /828,788A /94 MA75 NN: 11 LIBRARY OF FRANK	ALIGNMENTS	08-996-441B- 08-996-441B- 08-996-441B- 08-996-441B- 08-996-441B- 08-993-722A- 08-993-722A- 08-993-722A- 08-993-722A- 08-993-722A- 08-993-722A- 08-993-170A-
PTERA PESTS L FRANK GAERTNER		6664488664886648
NER STESS		Sequence 44, Sequence 60, Sequence 108 Sequence 108 Sequence 62, Sequence 64, Sequence 60, Sequence 60, Sequence 64, Sequence 62, Sequence 62, Sequence 68, Sequence 68,
		Appl Appl Appl Appl Appl Appl Appl Appl

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GENERAL INFORMATION:
APPLICANT: Fischhoff, David A.
APPLICANT: Fuchs, Roy L.
APPLICANT: Lavvik, Paul B.
APPLICANT: Lavvik, Paul B.
APPLICANT: McPherson, Sylvia A.
APPLICANT: Perlak, Frederick J.
TITLE OF INVENTION: Insect Resist.
NUMBER OF SEQUENCES: 2
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                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Lawrence M. Lavin,
STREET: 700 Chesterfield Parky
                                                                           ADDRESSEE:
STREET: 70
CITY: St. |
STATE: Mis
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                   ZIP: 63198
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Pred. No. 0;
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Best Local :
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ATFORMATION:
NAME: LAVIN JI, LAWIENCE M.
REGISTRATION NUMBER: 30,768
REFERENCE/DOCKET NUMBER: 38-2:
TELECOMMUNICATION INFORMATION:
TELEBHONE: (314) 537-7286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acid
TYPE: AMINO ACID
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APPLICATION NUMBER: 1
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,281
FILING DATE: 19930604
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YNSENLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
                                                     MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
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100.0%; Pred. No. 0;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (703) 836-20 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: JANSENS, STEIRAII
APPLICANT: PERFEROEN, Marnix
APPLICANT: PERFEROEN, MARNIX
TIVENTION: NEW DIABROTICA TOXINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 01
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CLASSIFICATION: 800
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 421 KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL 480
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                                                                                                                                                                                                                                                      IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS 180
                                       GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT
                                                      GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT 420
                                                                                                           RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS
                                                                                                                          RDVLTDPIVGVNNLRGYGTTESNIENYIRKPHLEDYLHRIQEHTREQPGYYGNDSENYWS
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P.O. Box 1404
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JANSENS, Stefan
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Pred. No. 0;
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GENERAL INFORMATION:
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                                                                                         Matches 644;
                                                                                                                     Query Match
                                                                                                                                                                                                                                          TELEFAX: (314) 537-604
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Relicurrent APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                   FILING DATE: 14-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lavin Jr., Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Insect Resistant Plants
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                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acid
                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (314) 537-7286
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                                                                                                                                                                                                                                                                                                     NAME: Lavin Jr., Lawrence M.
REGISTRATION NUMBER: 30,768
REFERENCE/DOCKET NUMBER: 38-21(10629)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 05
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                            TOPOLOGY:
                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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61 TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
                                                                                                     Match 100.0%;
Local Similarity 100.0%;
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                                                                                                                                                                                                           644 amino acids
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Perlak, Frederick J.
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                                                                                                       Score 644;
Pred. No. 0;
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                                                                                                                                                                              ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "'
          INFORMATION FOR SEQ
                ATTORNEY AGENT INFORMATION:
NAME: Patterson, Melinda L
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Perlak, Frederick J
TITLE OF INVENTION: Insect Resistant Plants
NUMBER OF SEQUENCES: 54
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fischhoff, Dan APPLICANT: Fuchs, Roy L APPLICANT: Perlak, Frede
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                                                                                                                                                                                                                                                                  CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-443
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                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 23-FEB-1998 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                               PO Box 4433
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          ID NO:
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                                                                                                                          Sequence 4, Application PC/TUS9211337
GENERAL INFORMATION:
APPLICANT: PAXNE, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS
TITLE OF INVENTION: ACTIVE AGAINST
NUMBER OF SEQUENCES: 16
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Best Local Similarity
                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID R. SALIWANCHIK
STREET: 2421 N.W. 41st STREET,
COMPUTER READABLE FORM
                     STREET: 2421 N.W. (
CITY: GAINESVILLE
STATE: FL
COUNTRY: USA
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TYPE: amino acid
STRANDEDNESS: not relevant
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Pred. No. 0;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.25

PCT/US92/11337

MEDIUM TYPE:

Floppy disk

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Best Local Similarity
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[INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: YE ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: BACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN: NIGERIENSIS INDIVIDUAL ISOLATE: IMMEDIATE SOURCE:
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TELEPHONE: 904-375-8100
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NAME: SALIWANCHIK, DAVID R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
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CLONE: 40D1
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                                                  KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL 480
                                                                                                                                   GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT 420
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 MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
                                                                                                   GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT
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                                  KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
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100.0%; Pred. No. 0;
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US-08-996-441B-113
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                                                                                                                                      Matches
                                                                                                                                                               Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM CCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:151
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 18-DEC CLASSIFICATION: 800
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COUNTRY: US
ZIP: 77210
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                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                             YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
                                          TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
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                          TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 128
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P.O. Box 4433
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                                                                                                                                    Conservative
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RESULT 8
US-08-993-722A-113
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: USCOB/993,722A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6060594
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 113,
                                                                                                                                                                                                                                                                                                                                APPLICANT: Von Tersch, Micha APPLICANT: Romano, Charles TITLE OF INVENTION: NUCLEIC TITLE OF INVENTION: COLEOPTE NUMBER OF SEQUENCES: 113 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                    ATTORNEY/AGENT INFORMATION:
NAME: KITCHELL Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MEC
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                     ADDRESSEE:
STREET: P.
CITY: Hous
STATE: Tex
                                                                                 APPLICATION NUMBER: FILING DATE: 18-DEC CLASSIFICATION: 43
                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
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Bryson, James W.
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                                                                                     18-DEC-1997
N: 435
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                                                                                                                                                    Release #1.0, Version #1
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US-08-993-170A-113
Sequence 113, Application US/08993170A
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF IN
                                                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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STRANDEDNESS:
TOPOLOGY: linear
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Local Similarity 100.0%;
nes 644; Conservative 0;
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                                                                                                                                                                                                                                                                                                                             YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT
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             Brussock, Susan M.
Malvar, Thomas M.
Bryson, James W.
Kulesza, Caroline A.
Walters, Frederick S.
Slatin, Stephen L.
Yon Tersch, Michael A.
                                                                                                                                English, Leigh H.
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 POLYPEPTIDE
                 Michael A.
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Pred. No. 0;
 COMPOSITIONS
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Best Local 9
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TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 113:
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TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: COLEOPTERAN INSECTS
                                                                                                                                                                                                                                                                                                                                                                           121 IADYAKNKALAELOGLQNIVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Arnold, White & Durkee
481 MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC 540
                                                                                                                                                    369 GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT 428
                                                                                                                                                                                                                           309 RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS 368
                                                                                                                                                                                                                                                 301 RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSENYWS 360
                                                                                                                                                                                                                                                                                                                        241 DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT 300
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                                                                                              421 KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL 480
                                                                                                                                                                                       361 GNYVSTRPSIGSNDIITSPFYGNKSSEPVONLEFNGEKVYRAVANTNLAVWPSAVYSGVT 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRWTADNNTEALDSS 68
                                                                                                                                                                                                                                                                                                      DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT 308
                                                                           KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL 488
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100.0%; Pred. No. 0;
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    Mismatches

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                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHODS FOR IMPROVING THE ACTIVITY OF TITLE OF INVENTION: DELTA-ENDOTOXINS AGAINST INSECT PESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Slatin, Stephen L.
APPLICANT: Von Tersch, Michael A.
TITLE OF INVENTION: METHODS FOR IMPROVING THE ACTIVITY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: ME
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Relaction CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                541 TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT 600
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                   121 IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 18-DE CLASSIFICATION: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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 181 MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                     69 TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 128
                                                                                                                                        61 TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
                                                                                                                                                                                                                                                              Match 100.0%; Score 644;
Local Similarity 100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                              1 MNDNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSS 60
                                                                                                                                                                           9 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEELRMTADNNTEALDSS 68
                                    IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS 188
                                                                                                                                                                                                                                                644; Conservative
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6077824
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                                                                                                                      652 amino acids
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                                                                                                                                                                                                                                                     0; Indels
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GENERAL INFORMATION:
                                                                                     APPLICATION NUMBER: US 08/057,191
FILING DATE: 03-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,844
FILING DATE: 28-JAN-1992
                                                                                                                                                                               CLASSIFICATION: 800
PRIOR APPLICATION UNABER: US 08/369,839
PRIOR APPLICATION (UNBER: US 08/369,839
PRIOR APPLICATION DATA:
               ATTORNEY/AGENT INFORMATION:
                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1000 Lo
CITY: Orlando
STATE: Florida
COUNTRY: USA
ZIP: 32801
                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 29-AUG
                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 GNYVSTRPSIGSNDIITSPFYGNKSSEÞVONLEFNGEKVYRAVANTNLAVWPSAVYSGVT 420
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1000 Legion Place, Suite 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adang, Michael J.
Rocheleau, Thomas A.
                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Merlo, Donald
                                 UMBER: US 07/242,482
09-SEP-1988
                                                                                                                                                                                                                                                                                   29-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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                                                                                                                                                                       ; Sequence 2, Application US/08705438
; Patent No. 6015891
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                                                                                                                                                     GENERAL INFORMATION:
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                                                                       APPLICANT: Rocheleau, Thomas A. APPLICANT: Merlo, Donald APPLICANT: Murray, Elizabeth E.
                                   TITLE OF INVENTION: Synt)
                                                                                                               APPLICANT:
APPLICANT:
CORRESPONDENCE ADDRESS:
                     NUMBER OF SEQUENCES:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 407-426-7500
                                                                                                                                                                                                                                                                             541 YEDKTINKGDTLTYNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN
                                                                                                                                                                                                                                                                                                 588 YFDKTINKGDTLTYNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
                                                                                                                                                                                                                                                                                                                                                                   481
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LENGTH: 597 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 AFMEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIR 167
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTN 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRLYPKEVKTELTRDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLEDYLHRIQFHTRFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRLYPKEVKTELTRDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLEDYLHRIQFHTREQ 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYKRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELFSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 92.7%; Score 597; DB 3; Length 597; Similarity 100.0%; Pred. No. 0;
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                                                                                                                                 Adang, Michael J.
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                                                   Synthetic Insecticidal Crystal Protein
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ADDRESSEE:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: MP TELECOMMUNICATION INFORMATION: TELEPHONE: 407-426-7500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 03-MAY-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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STREET: 1000 L
CITY: Orlando
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/369,839 FILING DATE: 06-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                   121 ELFSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAE 180
                                                                                                                                                                                                                                                                                                                                                                                108 AFMEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                         181 FYKROLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYD 240
                                                                                                                                                                                                                             228 FYKROLKLTOEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYD 287
                                                                                                                                                                                                                                                                                                                        168 ELFSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07 FILING DATE: 28-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 29-AU
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                408 LAVWPSAVYSGYTKVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEK 467
                                                      348 PGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTN 407
                                                                                                                                                     288 VRLYPKEVKTELTRDVLTDDIVGVNNLRGYGTTESNIENVIRKPHLFDYLHRIQFHTREQ 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 09-SE
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                                                                                                                                241 VRLYPKEVKTELTRDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 MTADNNTEALDSSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 35,589
                                                                                                                                                                                                                                                                                                                                                            61 AFMEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MTADNNTEALDSSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597;
E: Saliwanchik, Lloyd & Saliwanchik
1000 Legion Place, Suite 1750
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09-SEP-1988
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US-08-704-966-4
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Patent No. 601352
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              Query Match
                                                                                                                                                         INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 06-JAN-1995
PRIOR APPLICATION NUMBER: US 08/057,191
FILING DATE: 03-MAY-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA: US/08/704,966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 LAVWPSAVYSGYTKVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEK 420
                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 407-426-7500
TELEFAX: 407-839-8589
                                                                                                                                                                                                                 FILING DATE: 09-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/827,844
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                              MOLECULE TYPE:
                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 29
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/369,839 FILING DATE: 06-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/242,482 FILING DATE: 09-SEP-1988
                                                                             TOPOLOGY:
                                                                                          STRANDEDNESS:
                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Orlando
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                                                                                                                        610 amino acids
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Merlo, Donald
Murray, Elizabeth E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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                                                           protein
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92.4%; Score 595; D
100.0%; Pred. No. 0;
                                                                                                                                                                                                                                 35,589
                                                                                                                                                                                                                         MPS 8-88AFD3
                   DB 3;
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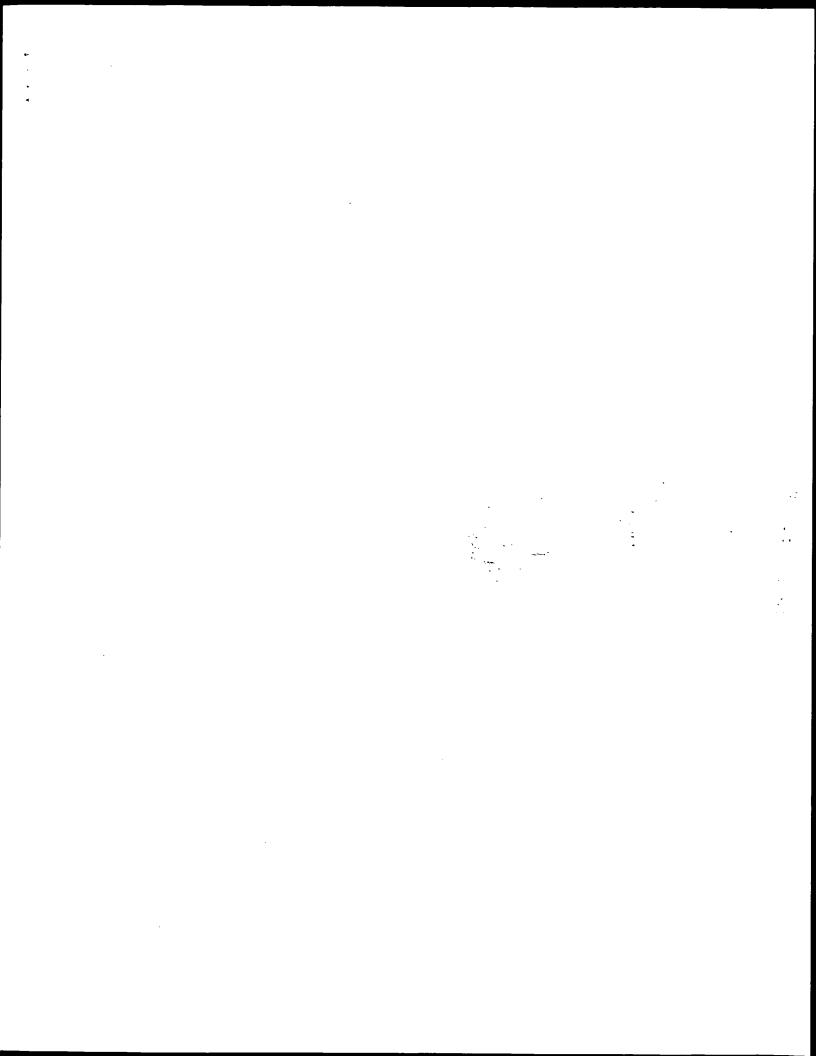
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US-08-705-438-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08705438 Patent No. 6015891
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                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,438
FILING DATE: 29-AUG-1996
                                                                                                                                                                                                                        STREET: 100 CITY: Orlando CTATE: Florida
            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                             APPLICANT: Merlo, Donald
APPLICANT: Murray, Elizabeth E.
TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
TITLE OF INVENTION: Gene
                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Adang, Michael J. APPLICANT: Rocheleau, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483
                                                 CLASSIFICATION:
                                                                                                                   OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            470 SHQLNYVMCFLMQGSRGTIFVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAG
                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 VWPSAVYSGVTKVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410 VWPSAVYSGYTKVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGY
                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350 YYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 LYPKEVKTELTRDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 KRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHQLNYVMCFLMQGSRGT1PVLTWTHKSVDFFNM1DSKK1TQLPLVKAYKLQSGASVVAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFY 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSQAESHERNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFY 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADNNTEALDSSTTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAF 62
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                                                                                                                                                                                                                                                                        1000 Legion Place,
                                                                                                        PatentIn Release #1.0, Version #1.30
                                                                                                                                IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                            Rocheleau, Thomas A.
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00 Leqion Place, Suite 1750
                                                                                                                                                                   Floppy disk
            us 08/369,839
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US-08-295-060-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                        543 DKTINKGDTLTYNSENLASESTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 597
                                                                             590 DKTINKGDTLTYNSENLASESTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
                                                                                                                            TYPE:
                                                                                                                                                                                                             423
                                                                                                                                                                                                                                              470
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                                                                                                                                                                                                                                                                                         410 VWPSAVYSGYTKVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGY 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 407-426-7500
                                                                                                                                                                                                                                                                                                                                                     303
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                                                                                                                                                                                                                                                                                                                                                                                                                                 290 LYPKEVKTELTRDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTREQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 KRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 KRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 FSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 FSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 MEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIREL 169
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/242,482 FILING DATE: 09-SEP-1988
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                                                                                                                                                   PRETGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYF
                                                                                                                                                                                                                       SHQLNYVMCFLMQGSRGT1PVLTWTHKSVDFFNM1DSKKITQLPLVKAYKLQSGASVVAG
                                                                                                                                                                                                                                                                    VWPSAVYSGVTKVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGY
                                                                                                                                                                                                                                                                                                                                        YYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLA
                                                                                                                                                                                                  SHQLNYVMCFLMQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAG
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Similarity 100.0%; Pred. No. 0;
95; Conservative 0; Mismatches
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Search completed: January 10, 2003, 11:11:25 Job time: 17 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:

NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-052
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VAN RIE, Jeroen
APPLICANT: JANSENS, Stefan
APPLICANT: PERFEROEN, Marnix
TITLE OP INVENTION: NEW DIABROTICA TOXINS
NUMBER OF SEQUENCES: 4
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LENGTH: 645 amino acids
TYPE: amino acid
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                  122 ADYAKNKALAELOGLQNNVEDYYSALSSWOKNPYSSRNPHSQGRIRELFSQAESHFRNSM 181
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STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                         63 TKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQKI 122
                                                                                                                                                                                                                                                                                                                                                                                          62 TKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQKI 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 NPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTEALDSST 61
                                                                    DVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTR 345
                                                                                                                                               HCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELTR 301
                                                                                                                                                                                                                         PSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYTD 241
                                                                                                                                                                                                                                                                                                 ADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNSM 182
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703) 836-2021
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Maximum DB seq length: 2000000000
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No.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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1332
US-10-120-544A-4
US-10-120-544A-8
US-10-120-544A-8
US-10-120-544A-8
US-10-120-544A-8
US-09-738-363-31
US-09-943-692-29
US-09-943-692-20
US-09-864-761-44452
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US-09-943-692-50
US-09-943-692-26
US-10-032-717-8
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US-09-943-692-53
US-09-943-692-3
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   Sequence 4, Appli
Sequence 4, Appli
Sequence 18, Appli
Sequence 6, Appli
Sequence 31, Appl
Sequence 29, Appl
Sequence 20, Appl
Sequence 20, Appl
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Sequence 53, Appl
Sequence 3, Appl1
Sequence 47, Appl
Sequence 50, Appl
Sequence 26, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 10, Appl
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US-10-032-717-2	US-09-826-660-23	US-09-756-526A-2	US-09-756-526A-4	US-09-738-626-5208	-881	US-10-032-717-40	US-10-032-717-22	US-10-032-717-12	US-10-032-717-44	US-10-032-717-24	US-10-032-717-16	US-10-032-717-10	US-10-032-717-6	US-09-738-626-5330	US-09-826-660-25	US-09-852-053-5	US-10-032-717-42	US-10-032-717-32	-10-032-	US-10-032-717-45	US-10-032-717-34	US-10-032-717-20		TG 00 00 00 00 00 00 00 00 00 00 00 00 00	rrs-09-886-055-249	US-09-816-669A-2
Sequence 2, Appli	Sequence 23, Appl	Sequence 2, Appli	4		Sequence Jos, App		5,) t			٠ - -	7 ,	5,	sequence Jose, ap	, i	<u>بر</u>			3 6	2	, .	7 6	3	N	Sequence 249, App	Sequence 2, Appli

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SEQ ID NO 2
LENGTH: 644
                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/027,998
PRIOR FILING DATE: 1998-02-23
NUMBER OF SEQ ID NOS: 54
SOFTWARF.
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                                                                                                                                                                  Matches 644;
                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MCPHERSON, SYLVIA A.
APPLICANT: PERLAK, FREDERICK J.
TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
FILE REFERENCE: MOBT:195--1
                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/943,692
CURRENT FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                     OTHER INFORMATION: Chimeric toxin
                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
61 TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYINFLNTIWPSEDPWKAFMEQVEALMDQK 120
                                                                                                           Similarity
                                                                                                                                                                     Conservative
                                                                                                                                                                                100.0%; Score 644;
100.0%; Pred. No. 0;
                                                                                                                                                                      0;
                                                                                                                                                                      Mismatches
                                                                                                                                                                                                   DB 10;
                                                                                                                                                                         0;
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                                                                                                                                                                                                  Length 644;
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1386 13 16 43 64 64

US-09-796-692-1601 US-09-796-692-1962 US-09-796-692-2485

Sequence Sequence sequence 1601, Ap sequence 1962, Ap sequence 2485, Ap

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RESULT 3
US-09-943-692-3
; Sequence 3, Application US/09943692
; Patent No. US20020152496A1
; GENERAL INFORMATION:
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APPLICANT: PERLAK, FREDERICK J.

TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS FILE REFERENCE: MOBT:195--1

FULRENT FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: 09/027,998

PRIOR APPLICATION NUMBER: 09/027,998

PRIOR FILING DATE: 1998-02-23

SOFTWARE: PATENTIN VETSION 3.1

SEQ ID NO 53

LENGTH: 20
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     APPLICANT: FISCHHOFF, DAVID A APPLICANT: FUCHS, ROY L.
                                                                                                                                                                                                                                Best Local
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APPLICANT:
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                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                         33 PNPTLEDLNYKEFLRMTADN 52
                                                                                                                                          1 PNPTLEDLNYKEFLRMTADN 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 MQGSRGTIPVLTWTHKSVDFFNMTDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 MOGSRGTIPVLTWTHKSVDFFNMIDSKKTTQLPLVKAYKLQSGASVVAGPRFTGGDIIQC 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 GNYVSTRPSIGSNDIITSPFYGNKSSEPVONLEFNGEKVYRAVANTNLAVWPSAVYSGVT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 RDVLTDPIVGVNNLRGYGTTFSNTENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 RDVLTDDIVGVUNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS 360
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Similarity 100.0%; Pred. No. 4.2e-13;
20; Conservative 0; Mismatches 0;
FUCHS, ROY L.
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LAVRIK, PAUL B.
                                                                                                                                                                                                                                Length 20;
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Sequence 50, Application US/09943692
Pattent No. US20020152496A1
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US-09-943-692-50
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                        GENERAL INFORMATION:

APPLICANT: FISCHHOFF, DAVID A.

APPLICANT: FUCHS, ROY L.

APPLICANT: LAVIE, PAUL B.

APPLICANT: MCPHERSON, SYLVIA A.

APPLICANT: PERLAK, FREDERICK J.

TITLE OF INVENTION: COLDEPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS

FILE REFERENCE: MOBT:195-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Bacillus thuringiensis US-09-943-692-47
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CURRENT APPLICATION NUMBER: US/09/943,692 CURRENT FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: FISCHHOFF, DAVID A.

APPLICANT: FUCHS, ROY L.

APPLICANT: LAVRIK, PAUL B.

APPLICANT: MCPHERSON, SYLVIA A.

APPLICANT: MCPHERSON, SYLVIA A.

APPLICANT: PERLAK, FREDERICK J.

TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS

FILE REFERENCE: MOBT:195-1

CURRENT APPLICATION UNMBER: US/09/943,692

CURRENT APPLICATION UNMBER: US/09/943,692

PRIOR APPLICATION UNMBER: 09/027,998

PRIOR APPLICATION UNMBER: 09/027,998

PRIOR FILING DATE: 1998-02-23

NUMBER OF SEQ ID NOS: 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 47
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PRIOR FILING DATE: 1998-02-23
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
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APPLICANT: MCPHERSON, SYLVIA A.
APPLICANT: PERLAK, FREDERICK J.
TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
FILE REFERENCE: MOBT:195-1 US/09/943,692
CURRENT FILING DATE: 2001-08-31
CURRENT FILING DATE: 2001-08-31
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100.0%; Pred. No. 2.5e-05;
vative 0; Mismatches 0;
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100.0%; Pred. No. 3.1e-08;
vative 0; Mismatches (
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TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-09-943-692-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Chimeric toxin US-09-943-692-26
                                                                                                                                                                                                                                                                                                                                                          US-10-032-717-8
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                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/10032717 Patent No. US20020151709A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: EUCHS, ROY L.

APPLICANT: LAVRIK, PAUL B.

APPLICANT: MCPHERSON, SYLVIA A.

APPLICANT: MCPHERSON, SYLVIA A.

APPLICANT: PERLAK, FREDERICK J.

APPLICANT: PERLAK, FREDERICK J.

FILE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS

FILE REFERENCE: MOBT:195-1

CURRENT APPLICATION NUMBER: US/09/943,692

CURRENT FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: 09/027,998

PRIOR FILING DATE: 1998-02-23

NUMBER OF SEQ ID NOS: 54

NUMBER OF SEQ ID NOS: 54
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    APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Sins
TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT APPLICATION NUMBER: 05/210/032,717
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                        APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Ronald D. Flannag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
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SEQ ID NOS: 48
                                                                                                                                                                                      Xiang Feng
Ronald D. Flannagan
Theodore W. Kahn
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Pred. No. 2.5e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 11; DB 10; pred. No. 0.00027;
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; LENGTH: 667
TYPE: PRT
ORGANISM: Bacillus thuringiensis (truncated)
US-10-032-717-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
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SEQ ID NO 18
LENGTH: 673
TYPE: PRT
ORGANISM: Bacillus thuringiensis (truncated)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.6%; Score 10; DB 12; Length 673; Best Local Similarity 100.0%; Pred. No. 0.098;
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                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10032717 Patent No. US20020151709A1
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TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
CURRENT FILING DATE: 2001-10-23
               ON GI DAS
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                                                                     APPLICANT: Lynn E. Sims
TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                   APPLICANT: Andre R. Abad APPLICANT: Nicholas B. I APPLICANT: Xiang Feng APPLICANT: Ronald D. Fli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                                 APPLICANT:
                                     SOFTWARE: FastSEQ for Windows Version 4.0
                                                          NUMBER OF SEQ ID NOS: 48
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LENGTH: 1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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Theodore W. Kahn
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                                                                                                                                                                                                                                                 Theodore W. Kahn
                                                                                                                                                                                                                                                                                                               Nicholas B. Duck
                                                                                                                                                                                                                                                                       Ronald D. Flannagan
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CURRENT APPLICATION NUMBER: US/10/120,544A
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-07-04
PRIOR FILING DATE: 2001-07-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 1316
TYPE: PRT
ORGANISM: BBCILLUS popilliae
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US-10-120-544A-4
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APPLICANT:
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Publication No. US20020182693A1
                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                               APPLICANT: NISHIHASHI, Hide]1
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or TITLE OF INVENTION: Insecticidal effect on scarabaeidae insects and TITLE OF INVENTION: poynucleotide encoding the same FILE REFERENCE: OP1335
CURRENT APPLICATION NUMBER: US/10/120,544A
CURRENT FILING DATE: 2002-04-12
CURRENT FILING DATE: 2002-04-12
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Best Local Similarity 100.0%; Pred. No. 0.1

Matches 10; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: JP 2001-203463
                       PRIOR APPLICATION NUMBER: JP 2001-115754 PRIOR FILING DATE: 2001-04-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NISHIHASHI, Hideji
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
TITLE OF INVENTION: poynucleotide encoding the same
FILE REFERENCE: OP1335
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APPLICANT: YOKOYAMA, Tomoko
APPLICANT: AOYAGI, Moriichi
APPLICANT: HASEGAWA, Makoto
APPLICANT: EHARA, Gaku
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KIMURA, Masaharu
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HASEGAWA, Makoto
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AOYAGI, Morlichi
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                     2001-04-13
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100.0%; Pred. No.
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0.18;
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RESULT 13
US-09-738-363-31
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LENGTH: 1332
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TANAKA, N
APPLICANT: YOKOYAMI
APPLICANT: AOYAGI,
APPLICANT: HASEGAWI
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CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: JP 2001-203463
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KIMURA, Masaharu
APPLICANT: NISHIHASHI, Hideji
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
TITLE OF INVENTION: poynucleotide encoding the same
FILE REFERENCE: OP1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
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TYPE: PRT
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                                                TITLE OF INVENTION: Nematicidal NUMBER OF SEQUENCES: 40 CORRESPONDENCE ADDRESS:
                                                                                                                                                                     APPLICANT: Schnepf, Harry E. Schwab, George E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
      ADDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TANAKA, Masao
YOKOYAMA, Tomoko
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                                                                                                                               Payne, Jewel M.
Narva, Kenneth E.
                                                                                                                 Foncerrada, Luis
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                                                                                            Proteins
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STATE: FL COUNTRY: U

USA

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PRIOR APPLICATION NUMBER: 09/027,998
PRIOR FILING DATE: 1998-02-23
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.1
SEQ ID NO 29
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 31: US-09-738-363-31
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                                      Query Match
Best Local Similarity
Thes 8; Conserva
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Best Local Similarity
"" Conservat
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                                                                                                                                         ; OTHER INFORMATION: Chimeric toxin US-09-943-692-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FISCHHOFF, DAVID A. APPLICANT: FUCHS, ROY L. APPLICANT: LAVRIK, PAUL B. APPLICANT: MCCHERSON, SYLVIA A. APPLICANT: PERLAK, FREDERICK J.
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PERLAK, FREDERICK J.
TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
FILE REFERENCE: MOBT:195-1
CURRENT APPLICATION NUMBER: US/09/943,692
CURRENT FILING DATE: 2001-08-31
CURRENT FILING DATE: 2001-08-31
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TELEFAX: 352-372-8800
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                               FEATURE:
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77 LGVVGFPF 84
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FILING DATE: 12-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/738,363
FILING DATE: 15-Dec-2000
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible operating SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-20CCCD3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                             Conservative
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                                                         1.2%; Score 8; DB 10;
100.0%; Pred. No. 0.26;
tive 0; Mismatches
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100.0%; Pred. No. 1e+05;
tive 0; Mismatches 0;
                                                         0; Indels
                                                                                                Length 13;
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LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
Search completed: January 10, 2003, 11:11:43
                                                                                                                                                                                                                   ; OTHER INFORMATION: Chimeric toxin US-09-943-692-20
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                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
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Patent No. US20020152496A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FUCHS, ROY L.

APPLICANT: LAVRIK, PAUL B.

APPLICANT: MCPHERSON, SYLVIA A.

APPLICANT: MCPHERSON, SYLVIA A.

APPLICANT: PERLAK, FREDERICK J.

TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FISCHHOFF, DAVID A. APPLICANT: FUCHS, ROY L.
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/027,998
PRIOR FILING DATE: 1998-02-23
NUMBER OF SEQ ID NOS: 54
                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/943,692
CURRENT FILING DATE: 2001-08-31
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                                                                                                        633 VYIDKIEF 640
                                                                       1 VYIDKIEF 8
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                                                                                                                                              Conservative
                                                                                                                                                         1.2%;
                                                                                                                                            0,
                                                                                                                                                             Score 8;
Pred. No.
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5. 0.31;
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OM protein - protein search, using sw model
Minimum DB seq length: 0
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Perfect score:
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                                                            Total number of hits satisfying chosen parameters:
                                                                                                 Word size :
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                                                                                                                                                                                                                                                                                                                        January 10, 2003, 11:08:29; Search time 21 Seconds (without alignments)
2948.122 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Database :

Post-processing: Listing first 45 summaries

PIR_73:*

pir1: *
pir2: *
pir3: *
pir4: *

SUMMARIES

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288	277	277	275	265	265	261	259	243	233	233	230	227	227	225	224
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C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:L03393; NID:g304150; PIDN:AAA22350.1; PID:g551698
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A; Residues: 9-58 < RE2>
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A;Experimental source: strain EG2158
R;Teixeira De Souza, M.; Lecadet, M.M.; Lereclus, D.
J. Bacteriol. 175, 2952-2960, 1993
A;Title: Full expression of the cryIIIA toxin gene of Bacillus thuringiensis requires A;Accession: I39813; MUID:93259939; PMID:8491716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 9-652 < RES>
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Mol. Gen. Genet. 214, 365-372, 1988
A;Title: Isolation and characterization of EG2158, a new strain of Bacillus thuringiens:
A;Reference number: I39812; MUID:89112139; PMID:3146015
A;Accession: I39812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Functional significance of loops in the receptor binding domain of Bacillus thu A;Reference number: S62317; MUID:96163559; PMID:8568902
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549 TENGSAATTYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPENQYYFDKTINKGDTLT
                       541 TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
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                                                                                                        MOGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC 540
                                                                                                                                                              KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL 488
                                                                                                                                                                                                                                              GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT 428
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100.0%; Pred. No. 0;
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C;Accession: S10228

R;Sick, A.; Gaertner, F.; Wong, A.
Nucleic Acids Res. 18, 1305, 1990

A;Title: Nucleotide sequence of a coleopteran-active toxin gene from a new isolate
A;Reference number: S10228; MUID:90206811; PMID:2320431
                                                                                                                        parasporal crystal protein cry3Bal - Bacillus thuringiensis (fragment)
N;Alternate names: coleopteran-active parasporal crystal protein; delta-endotoxin
C;Species: Bacillus thuringiensis
C;Date: 31-Dec_1993 #sequence_revision 31-Dec-1993 #text_change 01-Dec-2000
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A; Residues: 1-652 < RES>
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A;Title: Characterization of two genes encoding Bacillus thuringiensis insecticidal c A;Reference number: I39811; MUID:93119147; PMID:1476436
A;Accession: I39811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 01-Dec-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      parasporal crystal protein cry3Bbl - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cryIIIB2
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A;Title: Nucleotide sequence of gene cryIIID encoding a novel coleopteran-active crys
A;Reference number: JH0261; MUID:92184108; PMID:1544571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             parasporal crystal protein cry3Cal - Bacillus thuringiensis subsp. kurstaki (strain B N;Alternate names: parasporal crystal protein cryIIID c;Species: Bacillus thuringiensis subsp. kurstaki C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Dec-2000 C;Accession: JH2C61; S18944
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C:Superfamily: parasporal crystal protein
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A; Residues: 1-649 <LAM>
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JH0261
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100.0%; Pred. No
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A;Accession: S10228
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-659 <SIC>
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C;Keywords: delta-endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Structural similarity between the Lepidoptera- and Diptera-specific insecticide A;Reference number: A94672; MUID:86223796; PMID:3011746 A;Accession: B29838
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A;Residues: 1-1157 <LAM>
A;Residues: 1-1157 <LAM>
A;Cross-references: EMBL:Z37527; NID:g547554; PIDN:CAA85764.1; PID:g547556
A;Experimental source: serovar tolworthi
C;Comment: This parasporal crystal protein, active against corn borer and other insects,
C;Superfamily: parasporal crystal protein
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100.0%; Pred. No.
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b; Pred. No. 2.5
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              Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A; Accession: AC2045
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hypothetical protein BBJ24 - Lyme disease spirochete plasmid J/lp38 C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
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A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: A70248
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A; Residues: 1-260 <KLE>
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A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: D97340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA replication protein DnaC [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: D97340
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                                                A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AC2045
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Best Local Similarity
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A; Residues: 1-329 <KUR>
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                                                                                                                                   6-phosphofructokinase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.;
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100.0%; Pred. No.
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A; Residues: 1-483 <OLI>
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                                                                                                                                                                                                                                                                                                                                                                                                        probable integral membrane transport protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T36811
                                                                                                                                                                                                       A; Experimental source: strain A3(2)
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A; Accession: T36811
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A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: E75542
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C; Superfamily: t
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A; Residues: 1-375 <WHI>
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999  #sequence_revision 03-Dec-1999  #text_change 17-Mar-2000
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A;Nolecule type: DNA
A;Residues: 1-357 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73612.1; PID:g17131003; GSPDB:GN00179
A;Experimental source: Strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
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                                                                             Matches
                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Superfamily: thermophilic aminopeptidase I alpha chain
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                                  576 TLSLDGAP 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Per O.; Elsen, J.A.; Heldelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski,
                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        592 TINKGDTL 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 GDLLGVVG 81
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                                                                                                                                                                SCOEDB: SCI30A.31c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.0%;
                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                   Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Lhe EMBL Data Library, July 1999
                                                                           Conservative
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                                                                  100.0%; F1
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                                                                                         Score 8; ; Pred. No.
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C;Access.
R;Shevelev, A.B.; Svarr.
R;Shevelev, A.B.; Svarr.
R;Shevelev, A.B.; Svarr.
R;Shevelev, A.B.; Svarr.
                                                                C:Species: Bacillus thuringiensis
C:Date: 07-Oct.1994 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000
                                                                                                              parasporal crystal protein cry9Bal - Bacillus thuringiensis N;Alternate names: delta-endotoxin-related protein; paraspo
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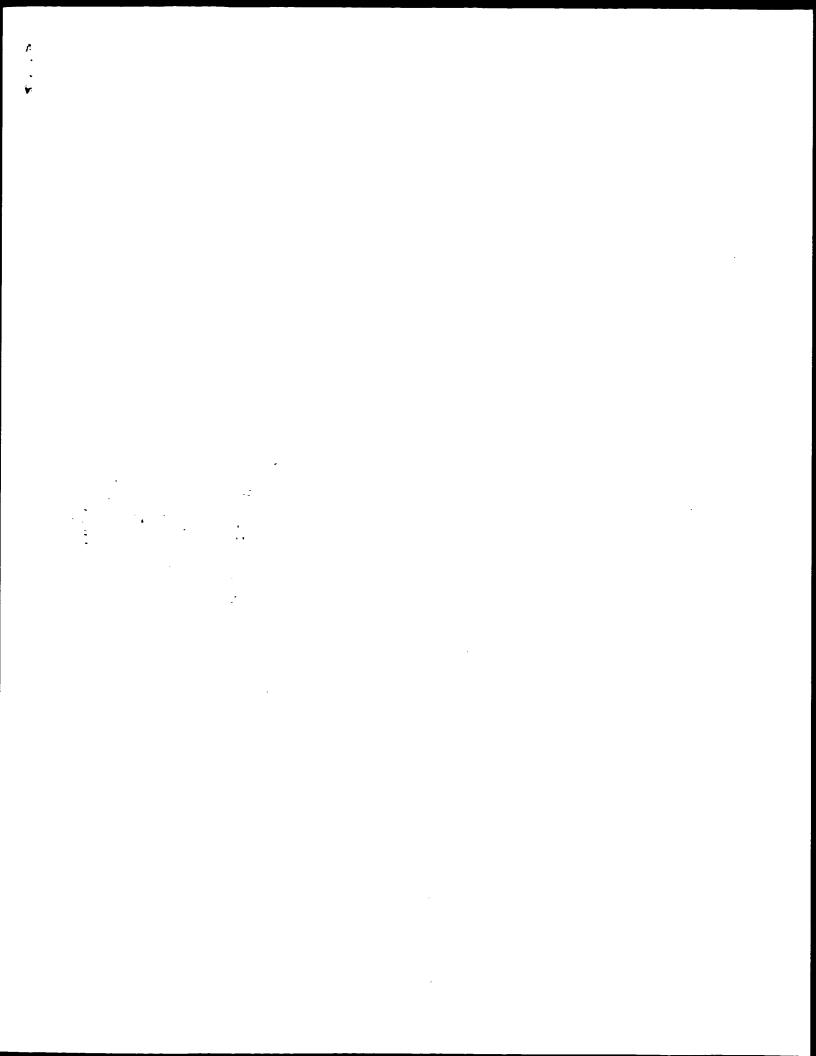
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A;Status: preliminary
A;Molecule type: DNA; protein
A;Molecules: 1-1138 <LAM>
                                                                                                                                                                               A;Cross-references: GB:M64478; NID:g142760; PIDN:AAA22351.1; PID:g142761
A;Note: sequence extracted from NCBI backbone (NCBIN:112092; NCBIP:112093)
C;Superfamily: parasporal crystal protein
                                                                                                                                                                      C; Keywords: delta-endotoxin
                                                                                                                                                                                                                                                                                                                                          A;Reference number: A48944; MUID:92384571; PMID:1514800
A;Contents: BT5137J
                                                                                                                                                                                                                                                                                                                                                                            R;Lambert, B.; Hofte, H.; Annys, K.; Jansens, S.; Soetaert, P.; Peferoen, M. Appl. Environ. Microbiol. 58, 2536-2542, 1992
A;Title: Novel Bacillus thuringiensis insecticidal crystal protein with a silent acti
                                                                                                                                                                                                                                                                                                                                A; Accession: A48944
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A; Residues: 1-760 <WIL>
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A; Accession: T24521
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                                                                                     Matches
                                                                                                                                 Query Match
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438 DSIDQLPP 445
                                           451 DSIDQLPP 458
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                                                                                                          Local
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mes 8; Conserv
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100.0%; Pr
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100.0%; Pred. No.
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Svarinsky, M.A.; Karasin, A.I.; Kogan, Y.N.; Chestukhina,

Ste

parasporal crystal protein cryx

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A;Title: Primary structure of the cryX, the novel delta-endotoxin-related gene from Baci A;Reference number: S39536; MUID:94085596; PMID:8262221
A;Accession: S39536
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1154 <SHE>
A;Cross-references: EMBL:X75019
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    parasporal crystal protein cry9Aal - Bacillus thuringiensis
N;Alternate names: delta-endotoxin; insecticidal crystal protein; parasporal crystal pro
C;Species: Bacillus thuringiensis
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 01-Dec-2000
C;Accession: S19306; S23588; A44847; S14602; S14837
R;Smulevitch, S.V.; Osterman, A.L.; Shevelev, A.B.; Kaluger, S.V.; Karasin, A.I.; Kadyrd
FEBS Lett. 293, 25-28, 1991
A;Reference number: S19306; MUID:92070568; PMID:1660003
A;Accession: S19306; MUID:92070568; PMID:1660003
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S19306
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R;Gleave, A.P.; Hedges, R.J.; Broadwell, A.H.
J. Gen. Microbiol. 138, 55-62, 1992
A;Title: Identification of an insecticidal crystal protein from
A;Reference number: A44847; MUID:92211329; PMID:1556556
A;Accession: A44847
Search completed: January 10, Job time : 24 secs
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                                                                                                                                                                                                                                                                                                                      A:Gene: cryIG
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin
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A;Residues: 1-1156 <SMU>
A;Residues: 1-1156 <SMU>
A;Cross-references: EMBL:X58120; NID:9870929; PIDN:CAA41122.1; PID:940271
A;Experimental source: subsp. galleriae
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A; Residues: 1-1151 <GLE>
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Best Local S
Matches 8
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                                                                                                                                                             267 RYRREMTL 274
                                                                                                                                                                                                               / Match 1.2%; Score 8; DB:
Local Similarity 100.0%; Pred. No. 28
mes 8; Conservative 0; Mismatches
                                                                                                            RYRREMTL 274
                           2003, 11:11:04
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5. 28;
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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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DB seq length: 2000000000
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644
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1907.911 Million cell updates/sec
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   Length DB
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CBBA_BACTP
COAA_BACTJ
CRAA_BACTO
CHAA_CLOBI
C7AA_BACTU
C7AB_BACTU
C7AB_BACTU
C7AB_BACUK
C9AA_BACTUK
C9A
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C3CA_BACTK
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CAAA_BACTI
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UXT_MOUSE
YJ10_MYCTU
TNF5_BOVIN
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TS22_HUMAN
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GILZ_RAT
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P07130; P21255;
01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry3Aa precursor (Insecticidal delta-endotoxin CryIIIA(a)) (Crystaline entomocidal protoxin) (73 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus thuringiensis (subsp. tenebrionis), Bacillus thuringiensis (subsp. morrisoni), and Bacillus thuringiensis (subsp. san diego).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1444, 1441, 1435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=B.t.tenebrionis;
MEDILINE=8015559; PubMed=3658680;
MOEFICH., Seurinck J., Houtven A.V., Vaeck M.;
Nucleotide sequence of a gene encoding an insecticidal protein of Bacillus thuringlensis var. tenebrionis toxic against Coleoptera.";
Nucleic Acids Res. 15:7183-7183(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sekar V., Thompson D.V., Maroney M.J., Bookland R.G., Adang "Molecular cloning and characterization of the insecticidal protein gene of Bacillus thuringiensis var. tenebrionis."; Proc. Natl. Acad. Sci. U.S.A. 84:7036-7040(1987).
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                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SPECIES-B. t. tenebrionis; STRAIN-NB176;
SPECIES-B. t. tenebrionis; STRAIN-NB176;
MEDILINE-95131759; PubMed-7830581;
Adams L.F., Mathewes S., O'Hara P., Petersen A., Gurtler H.;
Adams L.F., Mathewes S., O'Hara P., Petersen A., Gurtler H.;
Meluddation of the mechanism of CrylliA overproduction in a
mutagenized strain of Bacillus thuringiensis var. tenebrionis.";
Mol. Microbiol. 14:381-389(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-B.t.tenebrionis;
McPherson S.A., Perlak F.J., Fuchs R.L., Marrone P.G., Lavrik P.B.,
Fischhoff D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-B.t.tenebrionis;
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                                                                      SPECIES-B.t.morrisoni; STRAIN-EG2158;
MEDLINE-89112139; PubMed-3146015;
Donovan W.P., Gonzalez J.M. Jr., Gilbert M.P., Dankocsik C.C.;
Poolation and characterization of EG2158, a new strain of Bacillus
thuringiensis toxic to coleopteran larvae, and nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thuringlensis var. tenebrion
Biotechnology 6:61-66(1988).
                the toxin gene.";
Mol. Gen. Genet. 214:365-372(1988)
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Characterization of the coleopteran-specific protein gene of Bacillus thuringlensis var. tenebrionis.";
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CHAA_ECOLI
SUCC_PASMU
PYRC_SULSO
Y360_MYCGE
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DCDA_METTH
YWBA_BACSU
IRX2_MOUSE
UD18_RAT
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EMBL; J02978;
EMBL; M37207;
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EMBL;
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181 MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT 240
                              121 IADYAKNKALAELOGLONNVEDYVSALSSWOKNPVSSRNPHSQGRIRELFSQAESHFRNS
                                              121 IADYAKNKALAELOGLQNNVEDYVSALSSWOKNDVSSRNPHSOGRIRELFSQAESHFRNS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 353:815-821(1991).

-I- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT PRITHELIAL CELLS OF COLEOPTERA.

-I- DEVELOPMENTAL STACE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF THE SPORE COAT.
                                                                                                                                                                                                                                                                                                                                               Toxin; Sporulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                              ofam; PF00555; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li J., Carroll J., Ellar D.J.;
"Crystal structure of insecticidal delta-endotoxin from Bacillus thuringiensis at 2.5-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92049729; PubMed-1658659;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herrnstadt C., Gilroy T.E., Sobieski D.A., Bennett B.D.,
                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *Nucleotide sequence and deduced amino acid sequence of a coleopteran-
active delta-endotoxin gene from Bacillus thuringiensis subsp. san
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-88112860;
                                                                                                                                                                                   1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEELRMTADNNTEALDSS 60
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                                                                                            TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQK 120
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MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
                                                                                                            TTKDVIOKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWDSEDPWKAFMEQVEALMDQK 120
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A28407; A28407.
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A27323; A27323.
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1; AAA522541.1; -.
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                                                                                                                                                                                                                                                                                             3D-structure; Genetically modified food.
57 REMOVED IN MATURE FORM.
544 PESTICIDIAL CRYSTAL PROTEIN CRY3AA.
544 G -> A (IN REF. 3).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                           Lambert B., Theunis W., Aguda R., Van Audenhove K., Decock C., Jansens S., Seurinck J., Peferoen M.; "Nucleotide sequence of gene cryIIID encoding a novel coleopteranactive crystal protein from strain BTI109P of Bacillus thuringiensis subsp. kurstaki.";
                                                                                                                                                                                                                                EPITHELIAL CELLS OF COLEOPTERA.
-I- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92184108; PubMed-1544571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus thuringiensis (subsp. kurstaki).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein cry3Ca (Insecticidal delta-endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRY3CA OR CRYIIIC(A) OR CRYIIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CryIIIC(a)) (Crystaline entomocidal protoxin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q45744;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=29339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C3CA_BACTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 GNYVSTRPSIGSNDIITSPFYGNKSSEPVONLEFNGEKVYRAVANTNLAVWPSAVYSGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT 300
                                                                                                                                              SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                             MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
                                                                                                                                                                                                               SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
                                                                                                                                                                                                                                                             FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
                                                                                                                                                                         TERMINUS
                                                                                                                                                                                                          THE SPORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YNSFNLASFSTPFELSGNNLQIGYTGLSAGDKVYIDKIEFIPVN 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TENGSAATIYYTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQXYFDKTINKGDTLT 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOGSRGTIPVLTWTHKSVDFFNMIDSKKTTQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MQGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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RESULT
C3BB_B/
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THERE BERREADED SOCIO COCCOCCIO COCCOCCIO BERRARA REPRESENTA DE COCCOCCIO COCCOCCIO COCCOCCIO COCCOCCIO BERRARA REPRESENTA DE COCCOCCIO COCCOCIO COCCOCCIO COCCOCIO COCCOCCIO COCCIO COC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001178; Endotoxin.
Pfam; PF00555; endotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pesticidial crystal protein cry3Bb (Insecticidal delta-endotoxin cryIIIB(b)) (Crystaline entomocidal protoxin) (74 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C3BB_BACTU
                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-NRRL B-18655 / EG5144;
Donovan W.P., Rupar M.J., Slaney A.C.;
"Bacillus thuringlensis cryllic, (b) F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of two genes encoding Bacillus thuringiensis insecticidal crystal proteins toxic to Coleoptera species."; Appl. Environ. Microbiol. 58:3921-3927(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93119147; PubMed-1476436; Donovan W.P., Rupar M.J., Slaney Johnson T.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRY3BB OR CRYIIIB(B) OR CRYIIIB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 GYGTTFSNIENYIRKPHLFDYLH 338
                                                                                                           EMBL; U31633; AAA74198.1; -. HSSP; P07130; IDLC. InterPro; IPR001178; Endotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 GYGTTFSNIENYIRKPHLFDYLH 336
                                                                                                                                                                                             EMBL; M89794; AAA22334.1; -.
                               VARIANT
                                                          Toxin;
                                                                                 Pfam; PF00555; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              insects.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nt number US5378625, 03-JAN-1995.
FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF COLEOPTERA. HAS MODERATE LEVEL OF TOXICITY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE SPORE COAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOUTHERN CORN ROOTWORM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q45717;
                                                       Sporulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73026 MW;
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100.0%; Pred. No
        92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
  -> P (IN STRAIN EG5144).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 652 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein toxic to coleopteran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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Best Local
                                                       Query Match
                             Matches
                                            Best
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01-NOV-1990
01-NOV-1990
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30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein cry3Ba (Insecticidal delta-endotoxin cry1IB(a)) (Crystaline entomocidal protoxin) (75 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            Sick A., Gaertner F.H., Wong A.;
"Nucleotide sequence of a coleopteran-active toxin gene from a new isolate of Bacillus thuringlensis subsp. tolworthi.";
Nucleic Acids Res. 18:1305-1305(1990).
-I- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGI
                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus thuringiensis (subsp. tolworthi).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRY3BA OR CRYIIIB(A) OR CRYIIIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C3BA_BACTO
                                                                                                                                                      EMBL; x17123; CAA34983.1; -. EMBL; A07234; CAA00645.1; -. PIR; S10228; S10228.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-43F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 RIRELFSQAESHFRNSMPSFA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 RIRELFSQAESHFRNSMPSFA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90206811; PubMed=2320431;
                                                                                                             InterPro; IPR001178; Endotoxin Pfam; PF00555; endotoxin; 1.
                                                                                     SEQUENCE
                                                                                                  Toxin;
                                                                                                                                           HSSP; P07130;
                                                                                                                                                                                                                                                                                                                            - 1 - SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 165 RIRELFSQAESHFRNSMPSFA 185
                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                   EPITHELIAL CELLS OF COLEOPTERA.

DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                                                         OF THE SPORE COAT
                                                                                                                                                                                                                                                                                                                                              N-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                    SPORULATION AND IS ACCUMULATED BOTH AS
                                                                                                 Sporulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                            Similarity
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                             Conservative
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                                                                                                                                               1DLC
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352 F
419 V
451 S
590 L
600 K
624 K
74385 MW;
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                                                                                      75159 MW;
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F -> S (IN STRAIN EG5144).

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S -> G (IN STRAIN EG5144).

L -> I (IN STRAIN EG5144).

K -> I (IN STRAIN EG5144).

K -> T (IN STRAIN EG5144).
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; Pred. No.
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                                           Score 21;
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                                                                                      5A5B214FF84168CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     659 AA.
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                                              DB 1;
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                                              .2e-13
                                                                                                                                                                                                                                                                                                                                                                                       AN INCLUSION AND
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                                                          Length 659;
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DT 01-MAR
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DT 30-MAY
DE PESTLE
GN CTYYAA(
GN CTY10A
OS Bacili
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RP SEQUEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                     01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein cry10Aa (Insecticidal delta-endotoxin CryXA(a)) (Crystaline entomocidal protoxin) (78 kDa crystal protein).
CRY10AA OR CRYXA(A) OR CRYIYC.
Bacillus thuringiensis (subsp. israelensis).
Bacter1a: Firmicutes; Bacillales; Bacillaceae; Bacillus.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       P09662;
                                                                                                                                                                                                                                                                                                                                                                   CAAA_BACTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00555; endotoxin; 1. Toxin; Sporulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein).
CRY19AA OR CRYXIXA(A).
Bacillus thuringiensis (subsp. jegathesan).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              032307,
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidal crystal protein cry19Aa (Insecticidal delta-endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 WVNFNRYRREMTLTVLD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 WVNFNRYRREMTLTVLD 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001178; Endotoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROSSO M.L., Delectuse A.;
"Contribution of the 65-kilodalton protein encoded by the cloned gene
cry19A to the mosquitocidal activity of Bacillus thuringiensis subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CryXIXA(a)) (Crystaline entomocidal protoxin) (75 kDa crysta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98027382; PubMed-9361431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           )egathesan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CJAA_BACTJ
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DEVELOPMENTAL STAGE: THE CRYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. Environ. Microbiol. 63:4449-4455(1997).
FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF THE SPORE COAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P07130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y07603; CAA68875.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                648 AA;
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100.0%; Pred. No.
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                    -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Gill S.S.;
                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry25Aa (Insecticidal CryXXVA(a)) (Crystaline entomocidal protoxin) (76
                                                                                                                                                                                                                                                                                                                                                            087906;
16-0CT-2001 (Rel. 40,
                                                                     -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN
                                                                                                                                                                                                                                                         Bacteria;
                                                                                                                                                                                                                                                                  Bacillus thuringiensis (subsp. jegathesan)
                                                                                                                                                                                                                                                                                 protein) (Insecticidal protein Jeg74).
CRY25AA OR CRYXXVA(A).
                                                                                                                                                                                                                                                                                                                                                                                            CPAA_BACTJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 675 **
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InterPro; IPR001178; Endotoxin.
Pfam; PF00555; endotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                         NCBI_TaxID=56955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M12662; AAA22614.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-TERMINUS.
-1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thorne L., Garduno F., Thompson T., Decker D., Zounes M., Wild M., Walfield A.M., Pollock T.J.;
"Structural similarity between the lepidoptera- and diptera-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 EMTLTVLDLIA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 EMTLTVLDLIA 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                 EPITHELIAL CELLS OF INSECTS.

DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS
                                                                                           OF THE SPORE COAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                   Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   675 AA; 77760 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.7%; Score 11; DB 1; 100.0%; Pred. No. 0.008
                                                                                                             THE CRYSTAL PROTEIN IS PRODUCED DURING
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                                                                                                                                        BY BINDING TO THE MIDGUT
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Best Local
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Best Local
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16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                      Hwang S.H., Saitch H., Mizuki E., Higuchi K., Ohba M.;

A novel class of mosquitocldal delta-endotoxin, Cry19B, encoded
Bacillus thuringlensis serovar higo gene.";

Syst. Appl. Microbiol. 21:179-184(1998).

-i- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MI
EPITHELIAL CELLS OF MOSQUITOS;

-i- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS I
                                                                                                                     EMBL; D88381; BAA32397.1; -. HSSP; P07130; 1DLC.
InterPro; IPR001178; Endotoxin. Pfam; PF00555; endotoxin; 1.
Toxin; Sporulation; Plasmid.
                                                                                                                                                                                                                                   the European Bioinformatics Institute. They use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-98369730; Pubmed-9704107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pesticidial crystal protein cry19Ba (Insecticidal CryXIXB(a)) (Crystaline entomocidal protoxin) (78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CJBA_BACUH
086170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001178; Endotoxin.
Pfam; PF00555; endotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.lab-or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                           This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRY19BA OR CRYXIXB(A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein)
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                                                                                                                                                                                                                       entities
                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=132266
                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 RREMTLTVLDL
                          265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 RREMTLTVLDL 287
258
                                                                                                                                                                                                      tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                               OF THE SPORE COAT.
MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                     N-TERMINUS.
                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
FNRYRREMTL 267
                          FURYRREMTL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sporulation.
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                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                           Plasmid.
78490 MW;
                                               1.6%; but
100.0%; Pr
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                                                                  Score 10;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 11;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 509CC9F1F7501459 CRC64;
                                                                                                            5351EA63E2B042F7 CRC64;
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                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
0.0084;
                                                                                                                                                                                                                                                 There are no restrictions ng as its content is in
                                                                 0.088;
                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                            AN INCLUSION AND AS PART
                                                                                                                                                                                                                                      Usage
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                                                                               Length 682
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C8BA_BACUK
RRN OCCUPANT
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C9DA_BACTP
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                                                                                                                                                                                                                                                                                                                                                                    Best
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein cry9Da (Insecticidal delta-endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATENT NUMBER W09315206, 05-AUG-1993.

-IF FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF INSECTS. ACTIVE ON VARIOUS SCARABABID BEETLE:
-I- DEVELOPMENTAL STACE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry8Ba (Insecticidal delta-endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              045705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C8BA
                                                         CRY9DA OR CRYIXD(A). Bacillus thuringiensis Bacteria; Firmicutes; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRY8BA OR CRYVIIIB(A) OR 50C(B).
Bacillus thuringiensis (subsp. kumamotoensis).
Bacteria; Firmicutes; Bacillales; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CryVIIIB(a)) (Crystaline entomocidal protoxin) (134 kDa crystal
SEQUENCE FROM N.A:
STRAIN-N141;
                                                                                                                  CryIXD(a)) (Crystaline entomocidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U04365;
HSSP; P07130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                     protein)
                                                                                                                                                                                                            C9DA_BACTP
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001178; Endotoxin.
Pfam; PF00555; endotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Michaels T.E., Foncerrada L., Narva K.E., Process for controlling scarab pests wit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=NRRL B-18746 / PS50C;
                                          NCBI_TaxID=128936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                solates."
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                                                                                                                                                                                                                                                                                        272
                                                                                                                                                                                                                                                                                                                      269 RREMTLTVLD 278
                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-TERMINUS. SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF THE SPORE COAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACUK
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                                                                                                                                                                                                                                                                                                                                                                                                               1169 AA;
                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                         s (subsp. ja
Bacillales;
                                                                                                                                                                                                                                                                                                                                                                 1.6%; Score 10;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                             PRT;
                                                         japonensis).
≥s; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                               22EEFCF5BD699909 CRC64;
                                                                                                                  protoxin) (132
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0.14;
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                                                                                                                                                                                                                                 "Isolation and characterization of insecticidal genes fr
thuringiensis subsp. jegathesan.";
submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING T
EPITHELIAL CELLS OF INSECTS.
-I- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry24Aa (Insecticidal delta-endotoxin CryXXTVA(a)) (Crystaline entomocidal protoxin) (Crystal protein)
(Insecticidal protein Jeg72) (Fragment).
                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extrement and the Extra the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                               entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                 -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis (subsp. jegathesan).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  087905;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001178; Endotoxin. Pfam; PF00555; endotoxin; 1. Toxin; Sporulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Asano S.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Kawalek M.D., Gill S.S.;
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=56955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COAA_BACTJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF INSECTS.
DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF THE SPORE COAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                        OF THE SPORE COAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
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U88188;
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AAC61891.1;
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C9CA_BACTO
ID C9CA_BACTO
AC Q45733;
DT 30-MAY-2000
DT 16-OCT-2001
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CRAA_BACUH
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Best Local Similarity
Matches 9; Conserv
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Best Local :
                                                                                                                                                                                                                                                                                                         This SWISS-PROY entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                           Toxin;
                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                      InterPro; IPR001178; Endot
Pfam; PF00555; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE M
EPITHELIAL CELLS OF INSECTS.
-i- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "94kDa mosquitocidal toxin from serovar higo.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein).
CRY27AA OR CRYXXVIIA(A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry27Aa (Insecticidal delta-endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxin; Sporulation.
NON_TER 674
SEQUENCE 674 AA;
                                                                                                                                                                                                                                                                                EMBL; AB023293; BAA82796.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis (subsp. higo).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001178; Endotoxin.
Pfam; PF00555; endotoxin; 1.
                                                                                                                        674
                                                                                                                                                 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CryXXVIIA(a)) (Crystaline entomocidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9S597
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                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS:
                                                                                                                                    IDKIEFIPV
                                                                                                                                                                                                                                                                                                                                                                                                                              N-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF THE SPORE COAT
                                                                                                                        IDKIEFIPV
                                                                                                                                                                                                                                           Sporulation.
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9; Conserv
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(Rel.
(Rel.
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                                                     STANDARD;
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40,
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; 75959 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN
                                                                                                                                                                                                                             94434 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.4%;
                                                                                                                                                                                     1.4%; Score 9; I
100.0%; Pred. No.
                                                                                                                                                                                                                                                                     Endotoxin.
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                             DFD5313C5B6023E2 CRC64;
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Appl. Environ. Microbiol. 62:80-86(1996).

-I-FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGU EPITHELIAL CELLS OF LEPIDOPTERA LARVAE. HAS A FAIRLY BROAD SPECTRUM OF ACTIVITY AGAINST MEMBERS OF THE FAMILIES PYRALIDAE, PLUTELLIDAE, SPHINGIDAE, AND NOCTUIDAE. IT IS THE FIRST INSECTICIDAL CRYSTAL PROTEIN WITH ACTIVITY AGAINST CUTWORMS. NO ACTIVITY IS OBSERVED AGAINST SOME BEETLES, SUCH AS COLORADO POT
                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystatal-like protein cry17na (Insecticidal toxin CryXVIIA(a)) (Cbm72 mosquitocidal toxin).
CRY17na OR CRYXVIIA(A) OR CBM72.
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Bacteria; Firmicutes; Bacillales; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pesticidial crystal protein cry9Ca
CryIXC(a)) (Crystaline entomocidal
                   SEQUENCE FROM N.A.
STRAIN-CH18 / subsp. Malaysia;
MEDLINE-98267211; PubMed-96021
                                                                                                                                                                                    Clostridium bifermentans.
Bacteria; Firmicutes; Clo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001178; Endotoxin. Pfam; PF00555; endotoxin; 1. Toxin; Sporulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute. There are no restrictions on by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein cry7Aa (Insecticidal delta-endotoxin CryVIIA(a)) (Crystaline entomocidal protoxin) (129 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CRY7AA OR CRYVIIA(A) OR CRYIIIC.
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                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Bacteria; Firmicutes; Bacillales;
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DEVELOPMENTAL STAGE: PRODUCED DURING SPORULATION.
SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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Perfect score:
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                                                                                                                                                                                                                        Result
No.
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            January 10, 2003, 11:08:09; Search time 37 Seconds (without alignments) 3586.334 Million cell updates/sec
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7.8
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Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNPNNRSEHDTIKTTENNEV......TGLSAGDKVYIDKIEFIPVN 644
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_archea:*
sp_bacteria:*
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sp_bacteriap:*
sp_archeap:*
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                                                                                                                                                                                                                                                                                                                                                                                 sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                               sp_vertebrate:*
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 645
660
666
239
638
719
1254
138
2260
2294
329
329
329
                                                                                                                                                                                  Q9S6N9
P81518
                          Q9N6W1
6 050779
2 Q91FD3
7 Q97C11
6 Q97D92
                                                                                                      086287
087654
Q9F0P8
                                                                                                                                            Q9S603
Q8RQU6
Q8VW62
                                                                                            Q8VUL0
                                                                                                                                                                                                                                                                  SUMMARIES
                                                                           O9s6n9 bacillus th P81518 bacillus th O9s603 bacillus th O8rqu6 bacillus th O8c27 lactococcus O87654 bacillus th O9f0p8 bacillus th O9vulo bacillus th O9vulo bacillus th O9vulo bacillus th O9n6w1 drosphila
  O50779 borrella bu
Q91fd3 chilo iride
Q97c11 thermoplasm
Q97d92 clostridlum
Q8yvr1 anabaena sp
Q9rxs7 deinococcus
                                                                                                                                                                                                                            Description
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Osegno mus muscuito	Q9EQN0	11	201	1.1	7	45
drosc	Q9VGP7	σ	196	1.1	7	44
œ	Q8ZA68	16	194	1.1	7	43
homo sapie	Q9Y6E5	4	169	1.1	7	42
9 stre	Q9L0V9	16	163	1.1	7	41
	Q9X812	16	162	1.1	7	40
	Q8VEQ3	11	153	1.1	7	39
homo	Q96JS5	4	144	1.1	7	38
	Q8Y6P1	16	140	1.1	7	37
,	Q92B66	16	140	1	7	36
mus muscu	Q9EQN1	1	137	1.1	7	35
nomo	Q9NSM7	4	133	1.1	7	4
sum 6	Q9DC39	H	130	1.1	7	ω ω
sult	Q96Y21	17	114	1.1	7	3
	Q92EC3		89	 1	7	3
bacillus s	051815	N	85	1.1	7	w O
	061997		72	1.1	7	29
7 esche	Q8X9U7		57	1.1	7	28
ຜ	033956	N	3729		œ	27
	Q92225	w	1905	1.2	œ	8
	Q9NFV7	ഗ	1420		œ	ຣ
	Q8VUL1	N	1270	•	æ	24
bacillus	Q45745	N	1144	1.2	æ	3
drosophil	Q9VLY9	ഗ	798	1.2	œ	2
	Q22235	ഗ	760	•	œ	
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	Q8VQ48	N	485	1.2	&	ω:
Q9s242 streptomyce	098242	5	483	1.2	œ	7

ALIGNMENTS

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Best Local Similarity
Matches 644; Conserv
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Q9S6N9; PREVIOUS (TrembLrel 13, Created)
01-MAY-2000 (TrembLrel 13, Last sequence update)
01-JUN-2001 (TrembLrel 17, Last annotation update)
                                                                                                                                                                                                         Zhang J., Song F.P., Xie T.J., Wang K.M., Huang D.F.;
"A novel cry3Aa gene.";
submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ237900; CAB41411.1; -.
HSSP; P07130; 1DLC.
InterPro; IPR001178; Endotoxin.
Pfam; PF00555; endotoxin; 1.
SEQUENCE 652 AA; 74035 MW; 544AE16E1DDF7647 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Cry3Aa protein.
                                                                                                                                                                                                                                                                                                                                                                             Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                          STRAIN-BT22;
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1428;
                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
121 IADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNS
                                         9 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRWTADNWTEALDSS 68
                                                                                                                1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRWTADNNTEALDSS 60
                                                                                                                                                       Conservative
                                                                                                                                                       100.0%; Score 644;
100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                        Mismatches
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                                        Matches
                                                      Query Match
Best Local :
                                                                                                                                                                                                                        de Souza M., Lecadet M.M., Lereclus D.;
"Full expression of the cryllia toxin gene of Bacillus thuringiensis requires a distant upstream DNA sequence affecting transcription.";
J. Bacteriol. 175:2952-2960(1993).
-I- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
                                                                                                                                      TERMINUS.

EMBL; L03393; AAA22350.1; Interpro; IPRO01178; Endotox Pfam; PF00555; endotoxin; 1.
                                                                                                   SEQUENCE
                                                                                                                   NON TER
                                                                                                                                                                                                    -!- MISCELLANEOUS: TOXIC SEGMENT
                                                                                                                                                                                                                                                                                                          MEDLINE-93259939; PubMed-8491716;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-50 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
70 kDa CRYSTAL protein (Delta endotoxin) (CRYSTALINE ENTOMOCIDAL PROTECTION) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P81518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P81518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601 YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEEIPVN 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            489
1 MNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           429 KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFL 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 KVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVNCFL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 GNYVSTRPSIGSNDIITSPFYGNKSSEPVONLEFNGEKVYRAVANTNLAVWPSAVYSGVT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 MPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129
                                                                                                                                                                                                                    EPITHELIAL CELLS OF COLEOPTERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOGSRGTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TENGSAATIYVTPDVSYSOKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MQGSRGTIPVLTWTHKSVDFFNMIDSKKTTQLPLVKAYKLQSGASVVAGPRFTGGDIIQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDYLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTELT
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                                                                                                                             Sporulation.
                                                     Similarity
                                                                                              50 AA; 5829 MW;
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                            7.8%; Score 50;
100.0%; Pred. No.
                                                                                                                50
                                                                                                                                                        Endotoxin.
                                   0;
                                                                                         9AA1FD4DFCE7B808 CRC64;
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                                 Mismatches
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                                                DB 2; L
. 6.7e-45;
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                                                           Length 50;
                                Indels
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Q95603
ID Q956
AC Q956
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DT Q1-J
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                     "Cloning and Expression of Novel Crystal Protein Genes from Bacillus thuringiensis subsp. aizawai Encoding a Mosquitocidal Proteins."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB074413; BAB72016.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OBROUG:
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                   SEQUENCE
624 VYIDKIEFIP 633
                                              633 VYIDKIEFIP 642
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis
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                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1428
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insecticidal crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF042733; AAB97923.1; HSSP; P07130; IDLC.
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MEDLINE-99025985; PubMed-9806979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             516 ITQLPLVKAY 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *Assignment of delta-endotoxin genes of the four lepidoptera-specific Bacillus thuringiensis strains that produce spherical parasporal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wasano N., Ohba M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillaceae; Bacillus.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Delta-endotoxin (Fragment).
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                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                     Similarity
                                                                                                                                                                                           660 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001178; Endotoxin
                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           645 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                      75643 MW; A92EF6257C2B9404 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  645
                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72967 MW; 143E51312B890CE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                               1.6%; Score 10; DB 2
100.0%; Pred. No. 0.3;
                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bun2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                660 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          645 AA
                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
0.29;
                                                                                        0;
                                                                                                                                  Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 645;
                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                   <u>o</u>;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                0;
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RESULT 5
GNWAE2
ID WAW
AC QNWW
AC QNWW
AC QNWW
AC QNW
DT 01-W
DT 01-S
DE Inse
GN CRYEE
GN CRYEE
OS Bact
OC Bact
OC Bact
OC NCBB
RN [1]
RN [1]
RN Ito
OC NCBB
RT thub
RL Subb
RT Thirt
RL Subb
RT Intt
DR Intt
DR Intt
DR Intt
DR Intt
DR Intt
DR Pfan
DR Pfan
DR Pfor
DR NON
SQ SEQU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002
01-MAR-2002
01-JUN-2002
DNA Seq. 9:263-274 (1998).

EMBL; AJ000993; CAA04444.1; -.

InterPro: IPRO00160; GGDEF.

Pfam; PF00990; GGDEF: 1.

SMART; SM00267; DUF1: 1.

TIGRFAMS; TIGR00254; GGDEF; 1.

Hypothetical protein; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thuringiensis subsp. aizawai Encoding a Mosquitocidal Pr
Submitted (NOV-2011) to the EMBL/GenBank/DDBJ databases.
EMBL; AB074414; BAB72018.1: -.
InterPro; IPR001178; Endotoxin.
InterPro; IPR000834; Zn_carbOpept.
Pfam; PF00555; endotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8VW62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8VW62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insecticidal crystal protein bun3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         086287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ito T., Sahara K., Asano S., Bando H.;
"Cloning and Expression of Novel Crystal Protein Genes from
thuringlensis subsp. alrawal Encoding a Mosquitocidal Protei
                                                                                                      MEDLINE-99452385; PubMed-10524754;
Immonen T., Saris P.E.J.;
"Characterization of the nisfEG operon of the nisin Z Lactococcus lactis subsp. lactis N8 strain.";
The Company of the nisfEG operon of the nisin Z lactococcus lactis subsp. lactis N8 strain.";
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-NB; TRANSPOSON-TN5481;
MEDLINE-99452384; PubMed-10524753;
Immonen T., Wahlstroem G., Takala T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical 27.6 kDa protein.
                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-N8; TRANSPOSON-TN5481;
                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pLEB513
                                                                                                                                                                                                                                                    Immonen T., Wahlstroem G., Takala T., Saris P.E.J.;
"Evidence for a mosaic structure of the Tn5481 in L
                                                                                                                                                                                                                                                                                                                                                                Streptococcaceae; Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                              Lactococcus lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 RREMTLTVLD 278
                                                                                                                                                                                                                        DNA Seq. 9:245-261(1998).
                                                                                                                                                                                                                                                                                                                                               CBI_TaxID=1358;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RREMTLTVLD 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                666 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TremBLrel. 20, Created)
(TremBLrel. 20, Last sequence update)
(TremBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75311 MW; A87853FAE8FA4A1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M1smatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a Mosquitocidal Proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                group; Lactobacillales;
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                                                                                                                                                                                                                                                        in Lactococcus lactis
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                                                                                                                               producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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RESULT 7
087654
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Best Local Similarity
Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          087654;
01-NOV-1998
01-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=92-KU-149-8;
MEDLINE=21064760; PubMed=11136135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Two delta Endotoxin Genes, cry9Da and a Novel Related Gene, Commonly Occurring in Lepidoptera-Specific Bacillus thuringiensis Japanese Isolates That Produce Spherical Parasporal Inclusions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              087654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Delta-endotoxin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wasano N., Ohba M., Miyamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 TESNIENYI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 TFSNIENYI 328
                  Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF211190; AAG43526.1; . HSSP; P02965; 1CIY.
                                                                                                                                                                                                                                                  Bacillaceae;
                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                     Plasmid pBTC19
                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9F0P8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9F0P8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P07130; 1DLC
                                                                                      strain."
                                                                                                         Song F., Zhang J., Huang D., Li G.; "The cloning of a novel cryll gene from Bacillus thuringiensis
                                                                                                                                                        STRAIN-BTC
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                     NCBI_TaxID=1428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         509 ITQLPLVKA 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITQLPLVKA 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microbiol. 42:129-133(20 AF093107; AAC63366.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00555; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001178; Endotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 AA;
  IPR001178; Endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  638 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                  Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42:129-133(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71993 MW; 1817831FEF080A61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19,
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19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 9;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           %; Score 9; DB 2
%; Pred. No. 3.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96E3258044D233FD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          719
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   Query Match
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                                                              modifier mod(mdg4) in Drosophila.";
Genetics 155:141-157(2000)
                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Mod(mdg4)54.6 (Fragment).
MOD(MDG4) OR CG7836 OR CG8076 OR CG15802.
                         SEQUENCE
                                                        EMBL; AJ277178; CAB85473
                                                                                                           Buechner K., Roth P.,
                                                                                                                       SEQUENCE FROM N.A. MEDLINE-20253099;
                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                     "Genetic and molecular complexity of the
                                                                                                                                                                                                                                                                                Q9N6W1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Bacillus thuringiensis crystal protein gene.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB075461; BAB78602.1;
                                                                                                                                                                                                                                                                   29N6W1;
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Bacteria; Firmicutes; B
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nes 9; Conser
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les 9; Conserv
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                                           FBgn0002781; mod(mdg4).
                        138 AA;
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                                                                                                                       PubMed=10790390;
                   15414 MW; F8326FED60FC2C42 CRC64;
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1.2%;
                                                                                                      Schotta G., Krauss V., Saumweber H., Reuter G.,
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100.0%; Pred. No.
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100.0%; Pred. No.
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5;
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Best Local
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 MEDLINE-86174607; PubMed-3959991;
Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
"Insect iridescent virus type 6 induced toxic degenerative hepatitis
                                                                                        SEQUENCE FROM N.A.

Delius H., Darai G., Fluegel R.M.;

"DNA analysis of insect iridescent virus
permutation and terminal redundancy.";
                                                                                                                                                                                                                                                                    Q91FD3;
                                                                                                                                                                        Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus
in mice.";
                                                                                                                                                                NCBI_TaxID=10488;
                                                                                                                                                                                                                           01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR; BBJ24; -.
Hypothetical protein; Plasmid; Complete proteome.
SEQUENCE 260 AA; 30484 MW; B0102AFA88E5DCBE CRC64;
                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.;
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050779;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 35210 / B31;
MEDLINE=98065943; PubMed=9403685;
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STRAIN-ATCC 35210 / B31;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein BBJ24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000787; AAC66120.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia burgdorferi (Lyme disease spirochete).
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                                                                                Virol. 49:609-614(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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(TrEMBLrel. 19, Last sequence up
(TrEMBLrel. 21, Last annotation
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SEÕUENCE FROM N.A.

MEDLINE-94353641; PubMed-8073636;

Sonntag K.C., Schnitzler P., Koonin E.V., D

"Chilo iridescent virus encodes a putative
distinct family within the 'DEAD/H' superfa
evolution of large DNA viruses.";

Virus Genes 8:151-158(1994).
          Schnitzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J., Koonin E.V., Darai G.; "Insect iridescent virus type 6 encodes a polypeptide related to largest subunit of eukaryotic RNA polymerase II."; J. Gen. Virol. 75:1557-1567(1994).
                                                                                                                             Sonntag K.C., Schnitzler P., Janssen W., Da
"Identification of the primary structure ar
the genome of insect infdescent virus type
coordinates 0.310 and 0.347 (7990 bp).";
Intervirology 37:287-297(1994).
                                                                                                                                                                                                                                                                                                                                                                 "Identification of genes encoding zinc finger chromosomal HMG protein homologue, and a putat in the genome of Chilo iridescent virus."; Nucleic Acids Res. 22:158-166(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                             Schnitzler P., Hug M., Handermann Delius H., Darai C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.; "Identification of the gene encoding the major capsid protein of insect iridescent virus type 6 by polymerase chain reaction."; J. Gen. Virol. 74:873-879(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fischer M., Schnitzler P., Delius H., Darai G.;
"Identification and characterization of the repetitive
the genome of insect iridescent virus type 6.";
Virology 167:485-496(1988).
                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-95213160; PubMed-7698884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization of the third origin of insect iridescent virus type 6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Virology 160:66-74(1987).
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iridescent virus type 6:
the viral genome.":
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                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94167241; PubMed=8121799;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification and mapping DNA sequences of the genome Virus Genes 6:19-32(1992).
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                                                                                  MEDLINE=94292906; PubMed=8021587;
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des a putative helicase belonging
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Thermoplasma volcar.

Archaea.
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Q97C11;
Q1-OCT-2001
                                                      STRAIN-GSS1 / DSM 4299 / JCM 9571;
MEDIINE-20570466; PubMed-11121031;
Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.
Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K.,
Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki Nunoshiba T., Aramaki H., Makino S.-I., Higuchi S.
Paramaki H., Makino S., Higuchi S.
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Muller K., Tidona C.A., Bahr U., I
"Identification of a thymidylate:
Chilo iridescent virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bahr U., Tidona C.A., Darai G.;
"The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101 and 0.391; similarities in coding strategy be insect and vertebrate iridoviruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                            Thermoplasma volcanium. Archaea; Euryarchaeota; Thermoplasmataceae; The
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pfam; pF00096; zf-C2H2; 1.
DNA-binding; Zinc-finger.
SEQUENCE 294 AA; 34614 MW;
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"Analysis of the First Complete DNA Sequence of an Invertebrate
"Inidovirus: Coding Strategy of the Genome of Chilo Iridescent Virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virus Genes 18:243-264(1999).
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                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=50339;
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Jakob N.J., Mueller K.,
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AP000992; BAB59436.1; -. Pro; IPR001387; HTH_3.
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D7 01-JU
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Kaneko T., Nakamura Y., Kohara M., Kawan A., Kawashima K., Kimura T.,

Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kohara M., Matsumoto M., Murati A.,

Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

Yasuda M., Tabata S.;

"Complete genomic sequence of the filamentous nitrogen-fixing

"Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                             Q8YVR1 PRELIMINAN, Q8YVR1, Q8YVR1, Q8YVR1, Q8YVR1, Q1-MAR-2002 (TrEMBLrel. 20, Last seq. Q1-JUN-2002 (TrEMBLrel. 21, Last ann. Q1-Tremptokinase.
                                                                                                                                                                                                                                                                                                           Anabaena sp. (strain PCC Bacteria; Cyanobacteria; Cyanobacteria; NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
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STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; PubMed-11466286;

MCDLINE-21359325; PubMed-11466286;

MCDLING J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Glbson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.

Bennett G.N., Koonin E.V., Smith D.R.;
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Complete proteome.
SEQUENCE 329 AA; 38693 My
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SMART; SM00550; HTH_XRE; 1.
Hypothetical protein; Complete
SEQUENCE 326 AA; 36773 MW;
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18, Last sequence update)
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Nostocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 8; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
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D10685EEEC08C931 CRC64;
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                DNA Res. 8:205-213(2001).
EMBL; AP003587; BAB73612.1; -.
InterPro; IPR00023; Ppfruckinase.
Pfam; pF00335; PFK; 1.
PRINTS; PR00476; PHFRCTKINASE.
ProDom; PD000707; Ppffruckinase; 1.
PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
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SEQUENCE 357 AA; 38006 MW; 40A6C3C266A6E5D0 CRC64;
                                                                          592 TINKGDTL 599
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